



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 148190

TO: Phillip Gabel
Location: rem/3c70
Art Unit: 1644
Thursday, March 24, 2005

Case Serial Number: 10/018245

From: Alex Wacławiw
Location: Biotech-Chem Library
CM1-6A02
Phone: 308-4491

Alexandra.waclawiw@uspto.gov

Search Notes

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STIC-Biotech/ChemLib

148 190

mej

From: Gambel, Phillip
Sent: Saturday, March 19, 2005 9:43 AM
To: STIC-Biotech/ChemLib
Subject: 10 / 018,245 Fukuda

stic

RECEIVED
MAR 21 2005
STIC

please perform a Sequence and a Sequence Interference Search for

in Paper

10 / 018,245 Fukuda tnf-specific antibodies

SEQ ID NO: 1

SEQ ID NO: 2

SEQ ID NO: 3

SEQ ID NO: 4

SEQ ID NO: 5

SEQ ID NO: 6

thanx

phillip gambel
art unit 1644
272-0844

1644 mailbox 3c70

*****Point of Contact:
STAFF USE ONLY Alexandra Wacławiw
Technical Info. Specialist
Searcher: CM1 6A02 Tel: 308-4491
Searcher Phone: 2-
Date Searcher Picked up: _____
Date Completed: 10
Searcher Prep/Rev. Time: _____
Online Time: 12

Type of Search
NA#: _____ AA#: 6
Interference: ☒ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): CompuGen

21

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:54:17 ; Search time 75.9375 Seconds
(without alignments)
50.931 Million cell updates/sec

Title: US-10-018-245A-1
Perfect score: 59
Sequence: 1 GYFTMYGNM 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	59	100.0	10 2	AAW70611 Anti-VEGF
2	59	100.0	10 5	AAG80311 Anti-huma
3	59	100.0	10 5	ABP61180 Humanised
4	59	100.0	10 8	ADR89785 Anti-CD70
5	59	100.0	67 7	ADH62639 Mouse ant
6	59	100.0	70 7	ADH62638 Mouse ant
7	59	100.0	70 7	ADH62637 Mouse ant
8	59	100.0	92 2	AAW24529 Anti-Fact
9	59	100.0	92 5	AAU80997 Human ant
10	59	100.0	112 2	AAW24521 Anti-Fact
11	59	100.0	112 5	AAU80980 Human ant
12	59	100.0	115 4	AAW84740 Variable
13	59	100.0	116 4	AAW84739 Variable
14	59	100.0	116 5	AAW27830 Mouse KS
15	59	100.0	116 5	AAW27833 Mouse KS
16	59	100.0	116 5	AAW27837 Mouse KS
17	59	100.0	116 5	AAW27825 Mouse KS
18	59	100.0	116 5	AAW27826 Mouse KS
19	59	100.0	116 5	AAW27828 Mouse KS
20	59	100.0	116 5	AAW27832 Mouse KS
21	59	100.0	116 5	AAW27834 Mouse KS
22	59	100.0	116 5	ADG67541 KS antibo
23	59	100.0	116 5	ADG67537 KS antibo
24	59	100.0	116 5	ADG67543 KS antibo
25	59	100.0	116 5	ADG67531 KS antibo

26	59	100.0	116 5	ADG67533 KS antibo
27	59	100.0	116 5	ADG67539 KS antibo
28	59	100.0	116 5	ADG67529 KS antibo
29	59	100.0	116 5	ADG67535 KS antibo
30	59	100.0	116 5	AAE33431 Murine KS
31	59	100.0	116 5	AAE33433 Murine KS
32	59	100.0	116 5	AAE33418 Heavy cha
33	59	100.0	116 5	AAE33434 Murine KS
34	59	100.0	116 5	AAE33435 Murine KS
35	59	100.0	116 5	AAE33414 Murine KS
36	59	100.0	116 5	AAE33432 Murine KS
37	59	100.0	116 5	AAE33438 Murine KS
38	59	100.0	116 5	AAE33429 Murine KS
39	59	100.0	116 5	AAE33430 Murine KS
40	59	100.0	116 5	AAE33437 Murine KS
41	59	100.0	116 5	AAE33416 EPCAM ant
42	59	100.0	116 5	AAE33436 Murine KS
43	59	100.0	116 5	AAO30908 hu-KS ant
44	59	100.0	116 5	AAO30911 di-KS ant
45	59	100.0	117 2	AAW28750 Heavy cha
46	59	100.0	117 5	AAW28752 Heavy cha
47	59	100.0	117 5	AAW80317 Anti-huma
48	59	100.0	117 6	AAE33439 Murine KS
49	59	100.0	117 8	ADG34377 Humanised
50	59	100.0	117 8	ADG34374 Humanised
51	59	100.0	117 8	ADG34375 Humanised
52	59	100.0	117 8	ADG34376 Humanised
53	59	100.0	117 8	AD126496 Human BCL
54	59	100.0	118 2	AAW25412 Heavy cha
55	59	100.0	118 2	AAW25414 Heavy cha
56	59	100.0	118 2	AAW41284 Moderate-risk
57	59	100.0	118 2	AAW38615 Low-risk
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63	59	100.0	118 2	AAW70676 Anti-VEGF
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69	59	100.0	118 5	ABP61247 Humanised
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71	59	100.0	118 8	AD101229 Murine mo
72	59	100.0	118 8	AD101170 Murine mo
73	59	100.0	118 8	AD101230 Murine mo
74	59	100.0	118 8	AD101169 Murine mo
75	59	100.0	119 2	AAW70674 Anti-VEGF
76	59	100.0	119 3	AAW11998 Anti-cort
77	59	100.0	119 3	AAW11996 Anti-cort
78	59	100.0	119 3	AAW11995 Anti-IL-d
79	59	100.0	119 3	AAW11999 Anti-cort
80	59	100.0	119 3	AAW11997 Anti-cort
81	59	100.0	119 6	ABU89693 Human alp
82	59	100.0	119 6	ABU89695 Human alp
83	59	100.0	119 6	ABO10809 Alpha-2 a
84	59	100.0	119 6	ABO10807 Alpha-2 a
85	59	100.0	120 7	ABW61521 Murine RS
86	59	100.0	120 7	AAW24510 Anti-Fact
87	59	100.0	121 2	AAW24534 Anti-Fact
88	59	100.0	121 2	AAW24519 Mouse ant
89	59	100.0	121 2	AAW24511 Anti-Fact
90	59	100.0	121 3	AAW05901 F(ab)-12
91	59	100.0	121 3	AAW13390 Anti-VEGF
92	59	100.0	121 5	AAW80982 Mammalian
93	59	100.0	121 5	AAW81004 Mammalian
94	59	100.0	121 5	AAW80987 Mammalian
95	59	100.0	121 5	AAW80972 Murine BC
96	59	100.0	121 7	ABW61525 Humanised
97	59	100.0	123 2	AAW24533 Anti-Fact
98	59	100.0	123 2	AAW86808 Variable

99 59 100.0 123 2 AAW68607
100 59 100.0 123 2 AAW70617

AAW68607 Variable
AAW70617 Anti-VEGF

ALIGNMENTS

RESULT 1
ID AAW70611 standard; peptide; 10 AA.

XX AAW70611;

XX 27-JAN-1999 (first entry)

DE Anti-VEGF antibody heavy chain hypervariable region CDRH1.

KW Heavy chain hypervariable region; murine; humanised antibody;

KW anti-vascular endothelial growth factor antibody; anti-VEGF antibody;

KW VEGF-induced angiogenesis; tumour; retinal disorder;

KW age-related macular degeneration; diabetic retinopathy;

KW rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.

XX Synthetic.

XX Mus sp.

XX WO9845331-A2.

XX 15-OCT-1998.

XX 03-APR-1998; 98WO-US006604.

XX 07-APR-1997; 97US-00833504.

XX 06-AUG-1997; 97US-00908469.

XX (GETH) GENENTECH INC.

XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM,

XX WPI; 1998-568337/48.

XX New humanised antibody with affinity for vascular endothelial growth

XX factor - for treatment of tumours; retinal disease and other angiogenic

XX states; also related nucleic acid, vectors and transformed cells.

XX Claim 8; Page 79; 100pp; English.

XX The present sequence represents a heavy chain hypervariable region of the

XX murine anti-vascular endothelial growth factor (anti-VEGF) antibody. The

XX sequence is used to construct the humanised anti-VEGF antibody of the

XX invention. The humanised antibodies are used to inhibit VEGF-induced

XX angiogenesis, particularly for treating or preventing tumours (of any

XX type) and retinal disorders (e.g. age-related macular degeneration or

XX diabetic retinopathy). They can also be used to treat other conditions

XX that involve angiogenesis, e.g. rheumatoid arthritis, psoriasis,

XX atherosclerosis, Grave's disease, etc

XX Sequence 10 AA;

XX Query Match 100.0%; Score 59; DB 2; Length 10;

XX Best Local Similarity 100.0%; Pred. No. 0.0076;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 GYFTNYGMN 10

XX 1 GYFTNYGMN 10

XX RESULT 2

XX AAG80311

XX AAG80311 standard; peptide; 10 AA.

XX AAG80311;

XX AAG80311;

XX 18-FEB-2002 (first entry)

DE Anti-human TNF-alpha CDR-H1 peptide.

KW TNF-alpha; tumour necrosis factor-alpha; antibody; anti-human; CDR;

KW heavy chain; light chain; complementarity determining region; vasotrophic;

KW antiarthritic; neuroprotective; protozoacide; toxic shock syndrome;

KW rheumatoid arthritis; malaria; multiple sclerosis.

XX Homo sapiens.

XX WO200179298-A1.

XX 25-OCT-2001.

XX 18-APR-2001; 2001WO-JP033308.

XX 19-APR-2000; 2000JP-00117394.

XX (SUNR) SUNTORY LTD.

XX Fukuda Y, Nagahira K, Nakanishi T;

XX WPI; 2002-066345/09.

XX Novel heavy and light-chain polypeptides of chimeric and humanized

XX antibodies against human tumor necrosis factor alpha for low-

XX immunogenicity treatment of TNF-related diseases such as toxic shock

XX syndrome.

XX Claim 1a; Page 25; 36pp; Japanese.

XX This invention describes novel heavy chain and light chain polypeptides

XX or their fragments of a recombinant antibody to human TNF-alpha which

XX contain complementarity determining region (CDR) sequences. The products

XX of the invention have vasotrophic, antiarthritic, neuroprotective and

XX protozoacide activity. The antibodies act by neutralising TNF-alpha in

XX vivo. The antibodies are used for producing chimeric and humanised

XX antibodies that may be used for the treatment and prevention of TNF-alpha

XX associated diseases such as toxic shock syndrome, rheumatoid arthritis,

XX malaria and multiple sclerosis. The antibodies have low immunogenicity in

XX humans. This sequence represents the anti-human tumor necrosis factor-

XX alpha (TNF-alpha) heavy chain CDR1 designated CDR-H1

XX Sequence 10 AA;

XX Query Match 100.0%; Score 59; DB 5; Length 10;

XX Best Local Similarity 100.0%; Pred. No. 0.0076;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 GYFTNYGMN 10

XX 1 GYFTNYGMN 10

XX RESULT 3

XX ABP61180

XX ABP61180 standard; peptide; 10 AA.

XX ABP61180;

XX 20-SEP-2002 (first entry)

XX Humanised anti-VEGF antibody heavy chain variable domain, CDRH1.

XX Cytostratic; ophthalmological; humanised; antibody; anti-VEGF; VEGF;

XX vascular endothelial growth factor; angiogenesis inhibitor; tumour;

XX retinal disorder; intraocular neovascular disorder; heavy chain;

XX variable domain; CDRH1.

XX Homo sapiens.

XX Mus sp.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:57:11 ; Search time 20.1562 Seconds
(without alignments)
37.035 Million cell updates/sec

Title: US-10-018-245A-1
Perfect score: 59
Sequence: 1 GYFTNYGMW 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents_Aa:*
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3: /cgn2_6/ptodaca/1/1aa/6A_COMB.dep:*
4: /cgn2_6/ptodaca/1/1aa/6B_COMB.dep:*
5: /cgn2_6/ptodaca/1/1aa/PCTUS_COMB.dep:*
6: /cgn2_6/ptodaca/1/1aa/backfile1.dep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	92	3	US-08-783-853A-84
2	59	100.0	92	3	US-08-344-050-84
3	59	100.0	112	3	US-08-783-853A-20
4	59	100.0	112	3	US-09-344-050-20
5	59	100.0	118	1	US-08-425-336-124
6	59	100.0	118	1	US-08-425-336-126
7	59	100.0	118	1	US-08-488-113B-124
8	59	100.0	118	1	US-08-488-113B-126
9	59	100.0	118	1	US-08-477-484B-124
10	59	100.0	118	1	US-08-477-484B-126
11	59	100.0	118	1	US-08-107-669D-28
12	59	100.0	118	1	US-08-107-669D-29
13	59	100.0	118	1	US-08-107-669D-66
14	59	100.0	118	1	US-08-107-669D-67
15	59	100.0	118	1	US-08-472-788A-28
16	59	100.0	118	1	US-08-472-788A-29
17	59	100.0	118	1	US-08-472-788A-88
18	59	100.0	118	1	US-08-472-788A-89
19	59	100.0	118	1	US-08-477-531B-28
20	59	100.0	118	2	US-08-477-531B-29
21	59	100.0	118	2	US-08-477-531B-66
22	59	100.0	118	2	US-08-477-531B-67
23	59	100.0	118	2	US-08-646-360-124
24	59	100.0	118	2	US-08-646-360-126
25	59	100.0	118	2	US-08-082-842A-28
26	59	100.0	118	2	US-08-082-842A-29
27	59	100.0	118	2	US-08-082-842A-88

28	59	100.0	118	2	US-08-082-842A-89	Sequence 89, App1
29	59	100.0	118	3	US-08-839-765-124	Sequence 124, App
30	59	100.0	118	3	US-08-839-765-126	Sequence 126, App
31	59	100.0	118	3	US-09-136-389-124	Sequence 124, App
32	59	100.0	118	3	US-09-136-389-126	Sequence 126, App
33	59	100.0	118	3	US-09-610-838-124	Sequence 124, App
34	59	100.0	118	3	US-09-610-838-126	Sequence 126, App
35	59	100.0	118	4	US-09-440-781-96	Sequence 96, App1
36	59	100.0	118	4	US-09-711-485-124	Sequence 124, App
37	59	100.0	118	4	US-09-711-485-126	Sequence 126, App
38	59	100.0	119	3	US-08-933-983-78	Sequence 78, App1
39	59	100.0	119	3	US-08-933-983-80	Sequence 80, App1
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44	59	100.0	121	3	US-08-783-853A-111	Sequence 111, App
45	59	100.0	121	3	US-09-344-050-7	Sequence 7, App1
46	59	100.0	121	3	US-09-344-050-31	Sequence 31, App1
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48	59	100.0	121	3	US-09-344-050-111	Sequence 111, App
49	59	100.0	121	4	US-09-440-781-98	Sequence 98, App1
50	59	100.0	123	3	US-08-783-853A-109	Sequence 109, App
51	59	100.0	123	3	US-09-344-050-109	Sequence 109, App1
52	59	100.0	138	3	US-08-933-983-11	Sequence 11, App1
53	59	100.0	138	3	US-08-933-983-15	Sequence 15, App1
54	59	100.0	139	3	US-08-933-983-21	Sequence 21, App1
55	59	100.0	139	3	US-08-933-983-89	Sequence 89, App1
56	59	100.0	140	3	US-09-344-050-89	Sequence 89, App1
57	59	100.0	140	3	US-08-488-113B-147	Sequence 147, App
58	59	100.0	240	1	US-08-488-113B-148	Sequence 148, App
59	59	100.0	240	1	US-08-477-484B-147	Sequence 147, App
60	59	100.0	240	1	US-08-477-484B-148	Sequence 148, App
61	59	100.0	240	1	US-08-477-484B-148	Sequence 148, App
62	59	100.0	240	2	US-08-646-360-147	Sequence 147, App
63	59	100.0	240	2	US-08-646-360-148	Sequence 148, App
64	59	100.0	240	3	US-08-839-765-147	Sequence 147, App
65	59	100.0	240	3	US-08-839-765-148	Sequence 148, App
66	59	100.0	240	3	US-09-136-389-147	Sequence 147, App
67	59	100.0	240	3	US-09-136-389-148	Sequence 148, App
68	59	100.0	240	3	US-09-610-838-147	Sequence 147, App
69	59	100.0	240	3	US-09-610-838-148	Sequence 148, App
70	59	100.0	240	4	US-09-711-485-147	Sequence 147, App
71	59	100.0	240	4	US-09-711-485-148	Sequence 148, App
72	59	100.0	250	1	US-08-133-804-2	Sequence 2, App1
73	59	100.0	250	1	US-08-461-184-8	Sequence 8, App1
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83	59	100.0	422	4	US-08-356-786-16	Sequence 16, App1
84	59	100.0	622	2	US-08-569-147-76	Sequence 76, App1
85	59	93.2	140	3	US-08-569-147-82	Sequence 82, App1
86	55	93.2	140	3	US-08-569-147-82	Sequence 82, App1
87	55	93.2	160	4	US-09-318-786-35	Sequence 35, App1
88	54	91.5	115	3	US-08-483-749A-24	Sequence 24, App1
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90	54	91.5	230	4	US-10-071-485-102	Sequence 102, App
91	54	91.5	235	4	US-09-485-737B-93	Sequence 93, App1
92	54	91.5	240	3	US-10-071-485-93	Sequence 93, App1
93	54	91.5	240	3	US-09-485-737B-91	Sequence 91, App1
94	54	91.5	243	1	US-08-133-804-6	Sequence 6, App1
95	54	91.5	243	1	US-08-133-804-6	Sequence 6, App1
96	54	91.5	243	2	US-08-461-184-6	Sequence 6, App1
97	54	91.5	243	2	US-08-461-184-6	Sequence 6, App1
98	54	91.5	267	3	US-09-485-737B-2	Sequence 2, App1
99	54	91.5	267	4	US-10-071-485-2	Sequence 2, App1
100	54	91.5	468	3	US-09-485-737B-67	Sequence 67, App1

ALIGNMENTS

RESULT 1
US-08-783-853A-84
Sequence 84, Application US/08783853A
Patent No. 6005091
GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Gross, Mitchell
APPLICANT: Feuerstein, Giora
APPLICANT: Nichols, Andrew
APPLICANT: Padian, Eduardo
APPLICANT: Patel, Arunbhai
APPLICANT: Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
TITLE OF INVENTION: OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/783,853A
FILING DATE: 16-JAN-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/029,119
FILING DATE: 24-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-783-853A-84

Query Match 100.0%; Score 59; DB 3; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYFTNYGMN 10
| | | | | | | | | |
Db 3 GYFTNYGMN 12

RESULT 2
US-09-344-050-84
Sequence 84, Application US/09344050

Patent No. 5391299
GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Gross, Mitchell
APPLICANT: Feuerstein, Giora
APPLICANT: Nichols, Andrew
APPLICANT: Padian, Eduardo
APPLICANT: Patel, Arunbhai
APPLICANT: Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
TITLE OF INVENTION: OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/344,050
FILING DATE: 24-JUN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-09-344-050-84

Query Match 100.0%; Score 59; DB 3; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYFTNYGMN 10
| | | | | | | | | |
Db 3 GYFTNYGMN 12

RESULT 3
US-08-783-853A-20
Sequence 20, Application US/08783853A
Patent No. 6005091
GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Gross, Mitchell
APPLICANT: Feuerstein, Giora
APPLICANT: Nichols, Andrew
APPLICANT: Padian, Eduardo

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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:56:15 ; Search time 57.6562 Seconds
(without alignments)
57.427 Million cell updates/sec

Title: US-10-018-245A-1
Perfect score: 59
Sequence: 1 GYFTNYGMN 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 31100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA:*
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18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	ID	Description
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3	59	100.0	10	16	US-10-018-245A-1
4	59	100.0	10	16	US-10-723-434-112
5	59	100.0	10	16	US-10-723-434-116
6	59	100.0	67	14	US-10-243-130-19
7	59	100.0	70	14	US-10-243-130-17
8	59	100.0	70	14	US-10-243-130-18
9	59	100.0	70	17	US-10-901-650-17
10	59	100.0	70	17	US-10-901-650-18
11	59	100.0	70	17	US-10-901-650-19
12	59	100.0	92	9	US-09-965-099-84
13	59	100.0	92	13	US-10-051-852-84

14	59	100.0	92	15	US-10-430-176-84	Sequence 84, Appl1
15	59	100.0	112	9	US-09-965-099-20	Sequence 20, Appl1
16	59	100.0	112	13	US-10-051-852-20	Sequence 20, Appl1
17	59	100.0	112	15	US-10-430-176-20	Sequence 20, Appl1
18	59	100.0	116	9	US-09-971-543-9	Sequence 9, Appl1
19	59	100.0	116	9	US-09-971-543-8	Sequence 9, Appl1
20	59	100.0	116	9	US-09-971-543-10	Sequence 10, Appl1
21	59	100.0	116	14	US-10-138-727A-2	Sequence 2, Appl1
22	59	100.0	116	14	US-10-138-727A-4	Sequence 4, Appl1
23	59	100.0	116	14	US-10-138-727A-6	Sequence 6, Appl1
24	59	100.0	116	14	US-10-138-727A-17	Sequence 17, Appl1
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32	59	100.0	116	14	US-10-138-727A-25	Sequence 25, Appl1
33	59	100.0	116	14	US-10-138-727A-26	Sequence 26, Appl1
34	59	100.0	116	14	US-10-310-719-30	Sequence 30, Appl1
35	59	100.0	116	14	US-10-310-719-33	Sequence 33, Appl1
36	59	100.0	116	15	US-10-468-370-658	Sequence 658, Appl1
37	59	100.0	116	15	US-10-468-370-660	Sequence 660, Appl1
38	59	100.0	116	15	US-10-468-370-662	Sequence 662, Appl1
39	59	100.0	116	15	US-10-468-370-664	Sequence 664, Appl1
40	59	100.0	116	15	US-10-468-370-666	Sequence 666, Appl1
41	59	100.0	116	15	US-10-468-370-668	Sequence 668, Appl1
42	59	100.0	116	15	US-10-468-370-670	Sequence 670, Appl1
43	59	100.0	116	15	US-10-468-370-672	Sequence 672, Appl1
44	59	100.0	116	16	US-10-468-496-2021	Sequence 2021, Appl1
45	59	100.0	116	16	US-10-468-496-2022	Sequence 2022, Appl1
46	59	100.0	116	16	US-10-468-496-2023	Sequence 2023, Appl1
47	59	100.0	116	16	US-10-468-496-2025	Sequence 2025, Appl1
48	59	100.0	116	16	US-10-468-496-2027	Sequence 2027, Appl1
49	59	100.0	116	16	US-10-468-496-2029	Sequence 2029, Appl1
50	59	100.0	116	16	US-10-468-496-2031	Sequence 2031, Appl1
51	59	100.0	116	16	US-10-468-496-2033	Sequence 2033, Appl1
52	59	100.0	116	16	US-10-468-496-2035	Sequence 2035, Appl1
53	59	100.0	117	14	US-10-422-049-16	Sequence 16, Appl1
54	59	100.0	117	14	US-10-422-049-20	Sequence 20, Appl1
55	59	100.0	118	9	US-09-056-160B-104	Sequence 104, Appl1
56	59	100.0	118	9	US-09-056-160B-106	Sequence 106, Appl1
57	59	100.0	118	9	US-09-056-160B-108	Sequence 108, Appl1
58	59	100.0	118	14	US-10-268-883-9	Sequence 9, Appl1
59	59	100.0	118	14	US-10-127-890-124	Sequence 124, Appl1
60	59	100.0	118	14	US-10-127-890-126	Sequence 126, Appl1
61	59	100.0	118	14	US-10-234-671-7	Sequence 7, Appl1
62	59	100.0	118	14	US-10-234-671-102	Sequence 102, Appl1
63	59	100.0	118	14	US-10-234-671-104	Sequence 104, Appl1
64	59	100.0	118	14	US-10-234-671-106	Sequence 106, Appl1
65	59	100.0	118	14	US-10-422-049-15	Sequence 15, Appl1
66	59	100.0	118	14	US-10-422-049-19	Sequence 19, Appl1
67	59	100.0	118	15	US-10-340-189-28	Sequence 28, Appl1
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72	59	100.0	118	15	US-10-325-696-29	Sequence 29, Appl1
73	59	100.0	118	15	US-10-325-696-66	Sequence 66, Appl1
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75	59	100.0	118	15	US-10-624-153-96	Sequence 96, Appl1
76	59	100.0	118	17	US-10-683-043-9	Sequence 9, Appl1
77	59	100.0	118	17	US-10-683-043-14	Sequence 14, Appl1
78	59	100.0	118	17	US-10-717-243-124	Sequence 124, Appl1
79	59	100.0	118	17	US-10-717-243-126	Sequence 126, Appl1
80	59	100.0	119	8	US-08-934-000-78	Sequence 78, Appl1
81	59	100.0	119	8	US-08-934-000-80	Sequence 80, Appl1
82	59	100.0	119	10	US-09-977-283A-78	Sequence 78, Appl1
83	59	100.0	119	10	US-09-977-283A-80	Sequence 80, Appl1
84	59	100.0	120	15	US-10-377-121-9	Sequence 9, Appl1
85	59	100.0	120	15	US-10-377-121-9	Sequence 9, Appl1
86	59	100.0	121	9	US-09-965-099-7	Sequence 7, Appl1

87 59 100.0 121 9 US-09-965-099-31 Sequence 31, Appl
88 59 100.0 121 9 US-09-965-099-32 Sequence 52, Appl
89 59 100.0 121 9 US-09-965-099-111 Sequence 111, Appl
90 59 100.0 121 13 US-10-051-852-7 Sequence 7, Appl
91 59 100.0 121 13 US-10-051-852-31 Sequence 31, Appl
92 59 100.0 121 13 US-10-051-852-52 Sequence 52, Appl
93 59 100.0 121 13 US-10-051-852-111 Sequence 111, Appl
94 59 100.0 121 15 US-10-430-176-7 Sequence 7, Appl
95 59 100.0 121 15 US-10-430-176-31 Sequence 31, Appl
96 59 100.0 121 15 US-10-430-176-52 Sequence 52, Appl
97 59 100.0 121 15 US-10-430-176-111 Sequence 111, Appl
98 59 100.0 121 15 US-10-377-121-14 Sequence 14, Appl
99 59 100.0 121 15 US-10-624-153-98 Sequence 98, Appl
100 59 100.0 121 17 US-10-683-043-15 Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-09-056-160B-1

Sequence 1, Application US/09056160B
Patent No. US20020032315A1

GENERAL INFORMATION:

APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998

CLASSIFICATION: 424

PRIOR APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997

ATTORNEY/AGENT INFORMATION:
NAME: Haasak, Janet E.

REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-09-056-160B-1

Query Match 100.0%; Score 59; DB 9; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0038;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYFTNYGMN 10
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Db 1 GYFTNYGMN 10

RESULT 2

US-10-234-671-1

Sequence 1, Application US/10234671

Publication No. US20030190317A1

GENERAL INFORMATION:

APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.

TITLE OF INVENTION: ANTI-VEGF ANTIBODIES

NUMBER OF SEQUENCES: 131

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-Sep-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/056160

FILING DATE: 06-Apr-1998

APPLICATION NUMBER: 60/126446

FILING DATE: 07-Apr-1997

APPLICATION NUMBER: 60/054856

FILING DATE: 06-AUG-1997

ATTORNEY/AGENT INFORMATION:

NAME: Cui, Steven X.

REGISTRATION NUMBER: 44,637

REFERENCE/DOCKET NUMBER: P1093R2C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-234-671-1

Query Match 100.0%; Score 59; DB 14; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0038;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYFTNYGMN 10
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Db 1 GYFTNYGMN 10

US-10-018-245A-1

Sequence 1, Application US/10018245A

Publication No. US20040115196A1

GENERAL INFORMATION:

APPLICANT: FUKUDA, Yoshiaki

APPLICANT: NAKAMISHI, Toshihiro

APPLICANT: NAGAHIRA, Kazuhiro

TITLE OF INVENTION: Novel recombinant antibody, amino acid sequences of its complement

FILE REFERENCE: 46224

CURRENT APPLICATION NUMBER: US/10/018,245A

CURRENT FILING DATE: 2002-07-12

PRIOR APPLICATION NUMBER: JP 117394/2000

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:54:17 ; Search time 14.0625 Seconds
(without alignments)
68.421 Million cell updates/sec

Title: US-10-018-245A-1
Perfect score: 59
Sequence: 1 GYTFPTYGMN 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

PIR 79:.*
1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	59	100.0	105	2 S24764	Ig heavy chain V r
5	59	100.0	105	2 S24765	Ig heavy chain V r
6	59	100.0	109	2 S26325	Ig heavy chain V r
7	59	100.0	115	2 S19968	Ig heavy chain V r
8	59	100.0	115	2 S19965	Ig heavy chain V r
9	59	100.0	118	2 S19967	Ig heavy chain V r
10	59	100.0	119	2 A53285	Ig heavy chain V a
11	59	100.0	120	2 B42848	L6 mAb heavy chain
12	59	100.0	124	2 PH1404	Ig heavy chain V r
13	59	100.0	146	4 S33905	Ig heavy chain pre
14	55	93.2	140	2 A36194	Ig heavy chain V r
15	54	91.5	113	2 B36259	Ig heavy chain V r
16	54	91.5	119	2 PH1521	Ig heavy chain V r
17	54	91.5	119	2 PH1519	Ig heavy chain V r
18	54	91.5	136	2 S35759	Ig heavy chain V r
19	54	91.5	140	2 PH1489	BHD9D10 protein -
20	53	89.8	119	2 PH1516	Ig heavy chain V r
21	51	86.4	140	2 PH1488	Ig heavy chain V r
22	51	86.4	107	2 PH0987	Ig heavy chain V r
23	51	86.4	120	2 S12953	Ig heavy chain V r
24	50	84.7	76	2 B28572	Ig heavy chain V r
25	50	84.7	98	2 B24754	Ig heavy chain V r
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28	50	84.7	102	2 PH1490	Ig heavy chain V r
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31	50	84.7	114	2 PH1522	Ig heavy chain V r
32	50	84.7	118	2 S38565	Ig heavy chain V r
33	50	84.7	118	2 A24754	Ig heavy chain V r
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35	50	84.7	119	2 PH1505	Ig heavy chain V r
36	50	84.7	119	2 PH1518	Ig heavy chain V r
37	50	84.7	119	2 PH1517	Ig heavy chain V r
38	50	84.7	119	2 PH1502	Ig heavy chain V r
39	50	84.7	119	2 PH1500	Ig heavy chain V r
40	50	84.7	119	2 PH1503	Ig heavy chain V r
41	50	84.7	119	2 PH1504	Ig heavy chain V r
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43	50	84.7	121	2 A21854	Ig heavy chain V r
44	50	84.7	121	2 A26405	Ig heavy chain V r
45	50	84.7	123	2 G48677	Ig heavy chain V-D
46	50	84.7	123	2 F48677	Ig heavy chain V-D
47	50	84.7	123	2 E48677	Ig heavy chain V-D
48	50	84.7	134	2 S21916	Ig heavy chain V r
49	50	84.7	135	2 PH1494	Ig heavy chain V r
50	50	84.7	135	2 PH1492	Ig heavy chain V r
51	50	84.7	140	1 HYMS67	Ig heavy chain pre
52	50	84.7	140	2 PH1483	Ig heavy chain V r
53	50	84.7	140	2 PH1482	Ig heavy chain V r
54	49	83.1	98	2 S46460	Ig heavy chain V r
55	49	83.1	119	2 H45722	anti-glycoprotein
56	49	83.1	135	2 PH1493	Ig heavy chain V r
57	48	81.4	98	2 A49051	Ig heavy chain V7
58	48	81.4	105	2 S24763	Ig heavy chain V r
59	48	81.4	111	2 PH0988	Ig heavy chain V r
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61	48	81.4	116	2 S31667	Ig heavy chain V r
62	48	81.4	117	2 S31854	Ig heavy chain V r
63	48	81.4	117	2 S32190	Ig heavy chain V r
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65	48	81.4	142	2 S19245	Ig heavy chain pre
66	47	79.7	102	2 S42176	Ig gamma chain V r
67	47	79.7	102	2 C32530	Ig heavy chain V r
68	46	78.0	91	2 PH1004	Ig heavy chain V r
69	46	78.0	96	2 S17614	Ig heavy chain V r
70	46	78.0	96	2 S17613	Ig heavy chain V r
71	46	78.0	97	2 PH1155	Ig heavy chain V r
72	46	78.0	98	2 PH1106	Ig heavy chain V r
73	46	78.0	98	2 PH1144	Ig heavy chain V r
74	46	78.0	98	2 PH1151	Ig heavy chain V r
75	46	78.0	101	2 H37262	Ig heavy chain V r
76	46	78.0	103	2 PH0986	Ig heavy chain V r
77	46	78.0	106	2 S26315	Ig heavy chain V r
78	46	78.0	109	2 S26318	Ig heavy chain V r
79	46	78.0	110	2 S26317	Ig heavy chain V r
80	46	78.0	117	1 HYMS39	Ig heavy chain pre
81	46	78.0	117	2 G45722	anti-glycoprotein
82	46	78.0	118	2 C30560	Ig heavy chain V r
83	46	78.0	119	2 B32530	Ig heavy chain V r
84	46	78.0	119	2 PL0089	Ig heavy chain V r
85	46	78.0	120	2 A54256	Ig heavy chain V r
86	46	78.0	121	1 G1HDL	Ig heavy chain V-I
87	46	78.0	136	2 PL0208	Ig heavy chain pre
88	46	78.0	140	2 PH1484	Ig heavy chain V r
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90	45	76.3	94	2 G32513	Ig heavy chain V r
91	45	76.3	96	2 D25155	Ig heavy chain V r
92	45	76.3	98	2 S26913	Ig heavy chain V r
93	45	76.3	98	2 S26919	Ig heavy chain V r
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95	45	76.3	101	2 S42183	Ig gamma chain V r
96	45	76.3	109	2 PH0973	Ig heavy chain V r
97	45	76.3	111	2 S21925	Ig heavy chain V r
98	45	76.3	112	2 S09957	Ig heavy chain V-D
99	45	76.3	113	2 PH0974	Ig heavy chain V r
100	45	76.3	118	1 MHMS38	Ig heavy chain V r

ALIGNMENTS

RESULT 1

C24672
Ig heavy chain V region (VMU-1) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999

C/Accession: C24672

R/Winter, E.; Radbruch, A.; Krawinkel, U.

EMBO J. 4, 2861-2867, 1985

A/Reference number: A91022; MUID:86055722; PMID:2998759

A/Accession: C24672

A/Molecule type: DNA

A/Residues: 1-93 <WIN>

A/Cross-references: GB:X03300; NID:G52375; PIDN:CAA27039.1; PID:G773221

A/Note: this sequence was determined from the differentiated gene

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match Best Local Similarity 100.0%; Score 59; DB 2; Length 93;

Best Local Similarity 100.0%; Pred. No. 0.0018;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYFTNYGMN 10

Db 7 GYFTNYGMN 16

RESULT 2

S26326
Ig heavy chain V region - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 17-Apr-1998

C/Accession: S26326

R/Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A/Title: Antibodies that are specific for a single amino acid interchange in a protein

A/Reference number: S26309; MUID:91341421; PMID:1908510

A/Accession: S26326

A/Molecule type: mRNA

A/Residues: 1-99 <STA>

A/Cross-references: EMBL:X59174

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match Best Local Similarity 100.0%; Score 59; DB 2; Length 99;

Best Local Similarity 100.0%; Pred. No. 0.0019;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYFTNYGMN 10

Db 6 GYFTNYGMN 15

RESULT 3

D24672
Ig heavy chain V region (VGMW-8) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999

C/Accession: D24672

R/Winter, E.; Radbruch, A.; Krawinkel, U.

EMBO J. 4, 2861-2867, 1985

A/Reference number: A91022; MUID:86055722; PMID:2998759

A/Accession: D24672

A/Molecule type: DNA

A/Residues: 1-101 <WIN>

A/Cross-references: GB:X03300; NID:G51757; PIDN:CAA27040.1; PID:G773215

A/Note: this sequence was determined from the differentiated gene

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match Best Local Similarity 100.0%; Score 59; DB 2; Length 101;

Best Local Similarity 100.0%; Pred. No. 0.0019;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYFTNYGMN 10

Db 7 GYFTNYGMN 16

RESULT 4

S24764
Ig heavy chain V region (subgroup XI) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 20-Feb-1995 #sequence_revision 21-Nov-1998 #text_change 23-Jul-1999

C/Accession: S24764; S24772; S24777

R/Klares, S.

submitted to the EMBL Data Library, August 1992

A/Reference number: S24763

A/Accession: S24764

A/Molecule type: DNA

A/Residues: 1-105 <KLA>

A/Cross-references: EMBL:Z14999

A/Accession: S24772

A/Molecule type: DNA

A/Residues: 1-105 <KLM>

A/Cross-references: EMBL:Z15011

R/Thomas, J.W.

submitted to the EMBL Data Library, August 1992

A/Reference number: S24776

A/Accession: S24777

A/Molecule type: DNA

A/Residues: 1-105 <THO>

A/Cross-references: EMBL:Z15020; NID:G52616; PIDN:CAA78739.1; PID:G52617

C/Genetics:

A/Introns: 9/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match Best Local Similarity 100.0%; Score 59; DB 2; Length 105;

Best Local Similarity 100.0%; Pred. No. 0.002;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYFTNYGMN 10

Db 38 GYFTNYGMN 47

RESULT 5

S24765
Ig heavy chain V region (subgroup XI) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 20-Feb-1995 #sequence_revision 21-Nov-1998 #text_change 23-Jul-1999

C/Accession: S24765; S24773; S24778

R/Klares, S.

submitted to the EMBL Data Library, August 1992

A/Reference number: S24763

A/Accession: S24765

A/Molecule type: DNA

A/Residues: 1-105 <KLA>

A/Cross-references: EMBL:Z15001

A/Accession: S24773

A/Molecule type: DNA

A/Residues: 1-105 <KLM>

A/Cross-references: EMBL:Z15013

R/Thomas, J.W.

submitted to the EMBL Data Library, August 1992

A/Reference number: S24776

A/Accession: S24778

A/Molecule type: DNA

A/Residues: 1-105 <THO>

A/Cross-references: EMBL:Z15022; NID:G52619; PIDN:CAA78741.1; PID:G52620

C/Genetics:

A/Introns: 9/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:54:17 ; Search time 65.9375 Seconds
(without alignments)
77.661 Million cell updates/sec

Title: US-10-018-245A-1
Perfect score: 59
Sequence: 1 GYFTNYGMN 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

Uniprot 03:.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	91.5	241	2 Q921A6	Q921A6 mus musculus
2	50	84.7	120	1 HV021_MOUSE	P01747 mus musculus
3	50	84.7	140	1 HV021_MOUSE	P01746 mus musculus
4	49	83.1	125	2 Q6P1D0	Q6P1D0 homo sapien
5	46	78.0	117	1 HV59_MOUSE	P18530 mus musculus
6	46	78.0	121	1 HV3J_HUMAN	P01771 homo sapien
7	46	78.0	159	2 Q96QSO	Q96QSO homo sapien
8	46	78.0	481	2 Q91W73	Q91W73 mus musculus
9	46	78.0	485	2 Q6PDB8	Q6PDB8 mus musculus
10	45	76.3	118	1 HV51_MOUSE	P06330 mus musculus
11	45	76.3	140	2 Q65ZL3	Q65ZL3 mus sp. tgi
12	44	74.6	119	2 Q9GYZ2	Q9GYZ2 schistosoma
13	44	74.6	463	2 Q991C4	Q991C4 mus musculus
14	43	72.9	102	2 Q9JL79	Q9JL79 mus musculus
15	43	72.9	111	1 HV35_MOUSE	P01804 mus musculus
16	43	72.9	113	1 HV27_MOUSE	P01796 mus musculus
17	43	72.9	113	1 HV28_MOUSE	P01797 mus musculus
18	43	72.9	113	1 HV29_MOUSE	P01798 mus musculus
19	43	72.9	113	1 HV30_MOUSE	P01799 mus musculus
20	43	72.9	113	1 HV31_MOUSE	P01800 mus musculus
21	43	72.9	113	1 HV34_MOUSE	P01803 mus musculus
22	43	72.9	113	1 HV32_MOUSE	P01801 mus musculus
23	43	72.9	115	1 HV13_MOUSE	P01802 mus musculus
24	43	72.9	117	1 HV14_MOUSE	P01758 mus musculus
25	43	72.9	117	1 HV52_MOUSE	P06327 mus musculus
26	43	72.9	120	2 Q920E8	Q920E8 mus musculus
27	43	72.9	123	2 Q9V1J1	Q9V1J1 mus musculus
28	43	72.9	136	1 HV15_MOUSE	P01759 mus musculus
29	43	72.9	170	2 Q925S2	Q925S2 mus musculus
30	43	72.9	321	2 Q7ND50	Q7ND50 gloeobacter
31	43	72.9	475	2 Q6MZ06	Q6MZ06 homo sapien

32	43	72.9	484	2 Q991A6	Q991A6 mus musculus
33	43	72.9	487	2 Q80Z17	Q80Z17 mus musculus
34	42	71.2	121	1 HV01_MOUSE	P01745 mus musculus
35	42	71.2	498	2 Q6N041	Q6N041 homo sapien
36	42	71.2	1129	2 Q82N96	Q82N96 streptomyce
37	41	69.5	113	2 Q9UJ90	Q9UJ90 homo sapien
38	41	69.5	117	1 HV04_MOUSE	P01748 mus musculus
39	41	69.5	117	1 HV05_MOUSE	P01749 mus musculus
40	41	69.5	117	1 HV06_MOUSE	P01750 mus musculus
41	41	69.5	117	1 HV09_MOUSE	P01753 mus musculus
42	41	69.5	117	1 HV10_MOUSE	P01754 mus musculus
43	41	69.5	117	1 HV49_MOUSE	P06328 mus musculus
44	41	69.5	119	2 Q920E7	Q920E7 mus musculus
45	41	69.5	120	1 HV50_MOUSE	P06329 mus musculus
46	41	69.5	137	2 Q924R6	Q924R6 mus musculus
47	41	69.5	139	1 HV07_MOUSE	P01751 mus musculus
48	41	69.5	139	2 Q924R5	Q924R5 mus musculus
49	41	69.5	140	2 Q924P8	Q924P8 mus musculus
50	41	69.5	140	2 Q924R2	Q924R2 mus musculus
51	41	69.5	141	2 Q924Q4	Q924Q4 mus musculus
52	41	69.5	142	2 Q924Q1	Q924Q1 mus musculus
53	41	69.5	143	2 Q91V67	Q91V67 mus musculus
54	41	69.5	143	2 Q91VA2	Q91VA2 mus musculus
55	41	69.5	143	2 Q924P6	Q924P6 mus musculus
56	41	69.5	143	2 Q924Q5	Q924Q5 mus musculus
57	41	69.5	143	2 Q924R0	Q924R0 mus musculus
58	41	69.5	143	2 Q924R7	Q924R7 mus musculus
59	41	69.5	144	2 Q924P5	Q924P5 mus musculus
60	41	69.5	145	2 Q924P7	Q924P7 mus musculus
61	41	69.5	145	2 Q924Q6	Q924Q6 mus musculus
62	41	69.5	145	2 Q924Q7	Q924Q7 mus musculus
63	41	69.5	145	2 Q924Q9	Q924Q9 mus musculus
64	41	69.5	145	2 Q924R1	Q924R1 mus musculus
65	41	69.5	145	2 Q924R3	Q924R3 mus musculus
66	41	69.5	145	2 Q924R4	Q924R4 mus musculus
67	41	69.5	146	2 Q924Q3	Q924Q3 mus musculus
68	41	69.5	146	2 Q924R8	Q924R8 mus musculus
69	41	69.5	240	2 Q65ZC9	Q65ZC9 homo sapien
70	41	69.5	255	2 Q6K805	Q6K805 mus musculus
71	41	69.5	422	2 Q7UR28	Q7UR28 rhodospirell
72	41	69.5	473	2 Q9DB14	Q9DB14 mus musculus
73	41	69.5	473	2 Q91D05	Q91D05 mus musculus
74	41	69.5	482	2 Q8K172	Q8K172 mus musculus
75	41	69.5	482	2 Q840B9	Q840B9 mus musculus
76	41	69.5	488	2 Q8K0F2	Q8K0F2 mus musculus
77	41	69.5	613	2 Q8WUK1	Q8WUK1 homo sapien
78	40	67.8	109	2 Q9JL75	Q9JL75 mus musculus
79	40	67.8	118	2 Q9UJ91	Q9UJ91 homo sapien
80	40	67.8	122	1 HV3G_HUMAN	P01768 homo sapien
81	40	67.8	122	2 Q9UL84	Q9UL84 homo sapien
82	40	67.8	142	2 Q924Q2	Q924Q2 mus musculus
83	40	67.8	143	2 Q924P9	Q924P9 mus musculus
84	40	67.8	146	2 Q924Q8	Q924Q8 mus musculus
85	40	67.8	147	2 Q9Y509	Q9Y509 homo sapien
86	40	67.8	220	2 Q8RT26	Q8RT26 mus musculus
87	40	67.8	220	2 Q6X2M7	Q6X2M7 uncultured
88	40	67.8	220	2 Q6X2N8	Q6X2N8 uncultured
89	40	67.8	220	2 Q6X2N9	Q6X2N9 uncultured
90	40	67.8	220	2 Q6X2P0	Q6X2P0 uncultured
91	40	67.8	220	2 Q6X2P4	Q6X2P4 uncultured
92	40	67.8	220	2 Q6X2P6	Q6X2P6 uncultured
93	40	67.8	220	2 Q6X2P9	Q6X2P9 uncultured
94	40	67.8	220	2 Q6X2Q0	Q6X2Q0 uncultured
95	40	67.8	220	2 Q9AP60	Q9AP60 uncultured
96	40	67.8	220	2 Q9AP61	Q9AP61 uncultured
97	40	67.8	220	2 Q9AP62	Q9AP62 uncultured
98	40	67.8	220	2 Q9AP63	Q9AP63 uncultured
99	40	67.8	243	2 Q7TOM2	Q7TOM2 mus musculus
100	40	67.8	464	2 Q6MZ06	Q6MZ06 homo sapien

ALIGNMENTS

```

RESULT 1
ID HV02_MOUSE PRELIMINARY; PRT; 241 AA.
AC 0921A6
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DE Anti-CEA 79 single chain Fv (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scfv).";
RL Mol. Cells 7:816-819(1997).
DR EMBL: U88067; AAB48044.1; -
DR PIR: S19965; S19965.
DR PIR: S19967; S19967.
DR PIR: S19968; S19968.
DR PIR: S26325; S26325.
DR HSSP: P01607; 1BWM.
DR SMART: SM00406; IGV; 2.
DR PROSITE: PS50835; IG LIKE; 2.
FT NON_TER 1
FT NON_TER 241
SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match 91.5%; Score 54; DB 2; Length 241;
Best Local Similarity 90.0%; Pred. No. 0.13;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTNYGMN 10
Db 26 GYFTDYGMN 35

RESULT 2
ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8131846; PubMed=6186498;
RA Sikevitz M., Gelfer M.L., Brodeur P., Riblet R.,
Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idotype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -1- MISCELLANEOUS: From analysis of the sizes of several other
CC differentiatd genes that hybridize to this one, the authors
CC conclude that all of these V regions have rearranged to the same J
CC segment, JH2.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC PDB: 1JFQ; X-ray; H=1-120.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; IG; 1.
DR Pfam: PF00047; IG; 1.
DR SMART: SM00406; IGV; 1.
DR SMART; SM00406; IGV; 1.

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DR PROSITE: PS50835; IG LIKE; 1.
KW 3D-structure; Hybridoma; Immunoglobulin V region.
FT DOMAIN 1 111
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 84.7%; Score 50; DB 1; Length 120;
Best Local Similarity 80.0%; Pred. No. 0.33;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTNYGMN 10
Db 25 GYFTSYGIN 34

RESULT 3
ID HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A/J;
RX MEDLINE=92152818; PubMed=6801765;
RA Sims J., Rabbits T.H., Bates P., Slaughter C., Tucker P.W.,
Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J00493; AAA38128.1; -
DR PIR: A94264; HWMSC7.
DR HSSP: P01747; 1JFQ.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; IG; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
DR HydriDoma; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140
FT DOMAIN 20 139
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CB831D5C88 CRC64;

Query Match 84.7%; Score 50; DB 1; Length 140;
Best Local Similarity 80.0%; Pred. No. 0.38;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYFTNYGMN 10
Db 45 GYFTSYGIN 54

RESULT 4
ID Q6PIL0 PRELIMINARY; PRT; 125 AA.

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:54:17 ; Search time 129.094 Seconds
(without alignments)
50.931 Million cell updates/sec

Title: US-10-018-245A-2
Perfect score: 101
Sequence: 1 WINTYGEPTVADDFKG 17

Scoring table: BIOSUM62
Gapex 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 100 summaries

Database :

1: A_Geneseq_16Dec04:*
2: geneseqpl1980s:*
3: geneseqpl1990s:*
4: geneseqpl2000s:*
5: geneseqpl2001s:*
6: geneseqpl2002s:*
7: geneseqpl2003as:*
8: geneseqpl2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	101	100.0	17 5 AAG80312	Aag80312 Anti-huma
2	101	100.0	17 8 ADS87337	AdS87337 Humanised
3	101	100.0	19 2 AAY17490	Aay17490 Mab 31.1
4	101	100.0	19 2 AAY08699	Aay08699 Human col
5	101	100.0	19 3 AAY83642	Aay83642 Biotin Ia
6	101	100.0	67 7 ADH62639	Adh62639 Mouse ant
7	101	100.0	70 7 ADH62638	Adh62638 Mouse ant
8	101	100.0	112 7 ADC27441	Adc27441 TMERF2#18
9	101	100.0	112 7 ADC27449	Adc27449 TMERF2#21
10	101	100.0	115 4 AAB84740	Aab84740 Variable
11	101	100.0	116 4 AAB84739	Aab84739 Variable
12	101	100.0	116 5 AAE27830	Aae27830 Mouse KS
13	101	100.0	116 5 AAE27839	Aae27839 Mouse KS
14	101	100.0	116 5 AAE27837	Aae27837 Mouse KS
15	101	100.0	116 5 AAE27825	Aae27825 Mouse KS
16	101	100.0	116 5 AAE27826	Aae27826 Mouse KS
17	101	100.0	116 5 AAE27828	Aae27828 Mouse KS
18	101	100.0	116 5 AAE27832	Aae27832 Mouse KS
19	101	100.0	116 5 AAE27834	Aae27834 Mouse KS
20	101	100.0	116 5 ADG67541	Adg67541 KS antibo
21	101	100.0	116 5 ADG67537	Adg67537 KS antibo
22	101	100.0	116 5 ADG67543	Adg67543 KS antibo
23	101	100.0	116 5 ADG67531	Adg67531 KS antibo
24	101	100.0	116 5 ADG67533	Adg67533 KS antibo
25	101	100.0	116 5 ADG67539	Adg67539 KS antibo

26	101	100.0	116 5	ADG67529	Adg67529 KS antibo
27	101	100.0	116 5	ADG67535	Adg67535 KS antibo
28	101	100.0	116 6	AAE33431	Aae33431 Murine KS
29	101	100.0	116 6	AAE33433	Aae33433 Murine KS
30	101	100.0	116 6	AAE33434	Aae33434 Murine KS
31	101	100.0	116 6	AAE33435	Aae33435 Murine KS
32	101	100.0	116 6	AAE33414	Aae33414 Murine KS
33	101	100.0	116 6	AAE33432	Aae33432 Murine KS
34	101	100.0	116 6	AAE33438	Aae33438 Murine KS
35	101	100.0	116 6	AAE33430	Aae33430 Murine KS
36	101	100.0	116 6	AAE33437	Aae33437 Murine KS
37	101	100.0	116 6	AAE33436	Aae33436 Murine KS
38	101	100.0	116 6	AAO30908	Aao30908 hu-KS ant
39	101	100.0	116 6	AAO30911	Aao30911 di-KS ant
40	101	100.0	117 2	AAE28752	Aae28752 Heavy cha
41	101	100.0	117 5	AAE28751	Aae28751 Heavy cha
42	101	100.0	117 6	AAE33439	Aae33439 Murine KS
43	101	100.0	118 2	AAE25414	Aae25414 Heavy cha
44	101	100.0	118 8	ADN16150	Adn16150 Mouse C7
45	101	100.0	119 3	AAE11995	Aae11995 Anti-11-d
46	101	100.0	119 6	AAO23065	Aao23065 Murine K8
47	101	100.0	122 8	ADS87370	AdS87370 Chimeric
48	101	100.0	122 8	ADS87366	AdS87366 Murine MN
49	101	100.0	123 4	AAE98664	Aae98664 Murine pr
50	101	100.0	126 2	AAE17495	Aay17495 Heavy cha
51	101	100.0	137 5	AAE29158	Aae29158 Chimeric
52	101	100.0	138 6	AAO23064	Aao23064 Murine K8
53	101	100.0	138 7	ABR62341	AbR62341 Anti-HLA-
54	101	100.0	139 2	AAO9428	Aao9428 KM10 Heav
55	101	100.0	139 2	AAO6217	Aao6217 Mab KM10
56	101	100.0	139 2	AAE85064	Aae85064 Mouse KM1
57	101	100.0	139 6	ABU58898	Abu58898 Mouse ant
58	101	100.0	141 8	ADS87374	AdS87374 Humanised
59	101	100.0	240 8	ADN16154	Adn16154 Mouse C7
60	101	100.0	242 4	AAE20433	Aae20433 Anti-FLX/
61	101	100.0	259 7	ADG32324	Adg32324 Mouse scf
62	101	100.0	259 7	ADG32322	Adg32322 Mouse scf
63	101	100.0	329 7	ADG32359	Adg32359 Precursor
64	101	100.0	329 7	ADG32361	Adg32361 Precursor
65	101	100.0	447 1	AAE93037	Aae93037 Chimeric
66	101	100.0	579 6	AAE33444	Aae33444 KS antibo
67	101	100.0	579 6	AAO30910	Aao30910 di-KS-ala
68	98	97.0	160 4	AAE35101	Aae35101 Antibody
69	98	97.0	183 1	AAE70625	Aae70625 Sequence
70	98	97.0	183 1	AAE82936	Aae82936 Variable
71	98	97.0	183 1	AAE82938	Aae82938 Variable
72	98	97.0	183 1	AAE82939	Aae82939 Variable
73	98	97.0	183 2	AAE94778	Aae94778 V region
74	98	97.0	183 2	AAE10240	Aae10240 Variable
75	98	97.0	183 2	AAE10586	Aae10586 V region
76	98	97.0	183 2	AAE16341	Aae16341 L6 antibo
77	98	97.0	183 2	AAE41068	Aae41068 Mouse L6
78	98	97.0	183 2	AAE47511	Aae47511 Mouse L6
79	98	97.0	183 2	AAE47518	Aae47518 Mouse L6
80	98	97.0	183 2	AAE89536	Aae89536 Anti-canc
81	98	97.0	183 2	AAE89087	Aae89087 L6 VH CDN
82	98	97.0	183 7	ADC65008	Adc65008 Immunoglo
83	98	97.0	252 3	AAE12562	Aae12562 Chimeric
84	98	97.0	252 4	AAE36825	Aae36825 L6 sfv pr
85	97	96.0	17 7	ABR61518	AbR61518 Humanised
86	97	96.0	120 7	ABR61521	AbR61521 Murine RS
87	97	96.0	121 7	ABR61525	AbR61525 Humanised
88	97	96.0	469 7	ABR61529	AbR61529 Humanised
89	97	96.0	469 7	ABR61527	AbR61527 Humanised
90	97	96.0	509 5	AAU72872	Aau72872 3B10XP4-1
91	97	96.0	509 5	AAU72874	Aau72874 3B10XP5-2
92	97	96.0	503 5	AAU72873	Aau72873 Human NKG
93	97	96.0	505 5	AAU72875	Aau72875 Low-risk
94	96	95.0	118 2	AAE33615	Aae33615 Humanised
95	96	95.0	118 2	AAE38479	Aae38479 Humanised
96	96	95.0	118 2	AAE58516	Aae58516 Protein S
97	96	95.0	118 2	AAE58506	Aae58506 H65 prote
98	96	95.0	118 6	AAO23069	Aao23069 Murine an

99 96 95.0 118 8 ADI01229
100 96 95.0 118 8 ADI01170

Adi01229 Murine mo
Adi01170 Murine mo

ALIGNMENTS

RESULT 1

AAG80312
ID AAG80312 standard; peptide; 17 AA.

AC AAG80312;

XX 18-FEB-2002 (first entry)

XX Anti-human TNF-alpha CDR-H2 peptide.

XX TNF-alpha; tumour necrosis factor-alpha; antibody; anti-human; CDR;

KW heavy chain; light chain; complementarity determining region; vasotropic;

KW antiarthritic; neuroprotective; protozoacide; toxic shock syndrome;

KW rheumatoid arthritis; malaria; multiple sclerosis.

XX Homo sapiens.

XX WO200179298-A1.

XX 25-OCT-2001.

XX 18-APR-2001; 2001WO-JP003308.

XX 19-APR-2000; 2000JP-00117394.

XX (SUNR) SUNTORY LTD.

XX Fukuda Y, Nagahira K, Nakanishi T;

XX WPI; 2002-066345/09.

XX Novel heavy and light-chain polypeptides of chimeric and humanized

XX antibodies against human tumor necrosis factor alpha for low-

XX immunogenicity treatment of TNF-related diseases such as toxic shock

XX syndrome.

XX Claim 1b; Page 25; 36pp; Japanese.

XX This invention describes novel heavy chain and light chain polypeptides

XX or their fragments of a recombinant antibody to human TNF-alpha which

XX contain complementarity determining region (CDR) sequences. The products

XX of the invention have vasotropic, antiarthritic, neuroprotective and

XX protozoacide activity. The antibodies act by neutralising TNF-alpha in

XX vivo. The antibodies are used for producing chimeric and humanised

XX antibodies that may be used for the treatment and prevention of TNF-alpha

XX associated diseases such as toxic shock syndrome, rheumatoid arthritis,

XX malaria and multiple sclerosis. The antibodies have low immunogenicity in

XX human. This sequence represents the anti-human tumour necrosis factor-

XX alpha (TNF-alpha) heavy chain CDR1 designated CDR-H2

XX Sequence 17 AA;

XX Query Match 100.0%; Score 101; DB 5; Length 17;

XX Best Local Similarity 100.0%; Pred. No. 2.4e-08;

XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Db 1 WINTYTGEPTVADDFKG 17

XX 1 WINTYTGEPTVADDFKG 17

XX RESULT 2

XX ADS87337 standard; peptide; 17 AA.

XX AC ADS87337;

XX 18-NOV-2004 (first entry)

XX Humanised antibody MN3 heavy chain variable region CDR2.

XX cytotaxtic; vasotropic; antimicrobial; antiinflammatory; antipyretic;

KW antiatherosclerotic; cardiant; monoclonal antibody; NCA90; NCA95;

KW chimeric antibody; humanized antibody; inflammation; appendicitis;

KW inflammatory bowel disease; pelvic inflammatory disease; fever;

KW cystic fibrosis; granulocyte related disorder; atherosclerosis;

KW infarction; cancer; ischemic lesion; complementarity determining region.

XX Homo sapiens.

XX Mus sp.

XX Chimeric.

XX WO2004029093-A2.

XX 08-APR-2004.

XX 30-SEP-2003; 2003WO-GB004229.

XX 30-SEP-2002; 2002US-0414341P.

XX (IMMU-) IMMUNOMEDICS INC.

XX (MCCA/) MCCA L J D.

XX Goldenberg DM, Hansen H, Leung S;

XX WPI; 2004-329873/30.

XX Monoclonal anti-granulocyte antibody that binds NCA90 and NCA95 antigens,

XX useful for treating malignancy, inflammation, atherosclerosis,

XX infarction, or other granulocyte related disorders.

XX Claim 4; Page 105; 134pp; English.

XX The invention relates to a monoclonal antibody (Mab) (I) or its fragment

XX that binds NCA90 or NCA95, where when the Mab or its fragment binds NCA90

XX the Mab or its fragment is chimeric, partially humanized or fully

XX humanized and where when the Mab or its fragment binds NCA95 the Mab or

XX its fragment is either fully humanized or chimeric, partially humanized

XX or fully humanized BW 250/183. (I) is useful for treating, detecting or

XX imaging sites of inflammation resulting from appendicitis, inflammatory

XX bowel disease, pelvic inflammatory disease, fever and cystic fibrosis and

XX treating granulocyte related disorders, atherosclerosis and infarction.

XX (I) is useful for detecting or treating cancer or ischemic lesion. This

XX sequence corresponds to the complementarity determining region 2 (CDR2)

XX of the heavy chain of the antibody of the invention.

XX Sequence 17 AA;

XX Query Match 100.0%; Score 101; DB 8; Length 17;

XX Best Local Similarity 100.0%; Pred. No. 2.4e-08;

XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Db 1 WINTYTGEPTVADDFKG 17

XX 1 WINTYTGEPTVADDFKG 17

XX RESULT 3

XX AA17490 standard; peptide; 19 AA.

XX ID AA17490

XX AC AA17490;

XX 03-AUG-1999 (first entry)

XX Mab 31.1 CDR sequence derived peptide COL311 H2.

XX Heavy chain variable region; 2CAVHCOL1; light chain variable region;

XX light chain consensus region; heavy chain consensus region; antibody;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:57:11 ; Search time 34.2656 Seconds
(Without alignments)
37.035 Million cell updates/sec

Title: US-10-018-245A-2
Perfect score: 101
Sequence: 1 WINTYGEPTVADDFKG 17

Scoring table: BLOSUM62
Gapext 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCrUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	98	97.0	160	4 US-09-318-786-35	Sequence 35, Appl
2	98	97.0	252	3 US-08-279-772A-6	Sequence 6, Appl
3	98	97.0	252	3 US-08-902-486-9	Sequence 9, Appl
4	96	95.0	118	1 US-08-425-336-124	Sequence 124, App
5	96	95.0	118	1 US-08-488-113B-124	Sequence 124, App
6	96	95.0	118	1 US-08-477-484B-124	Sequence 124, App
7	96	95.0	118	1 US-08-107-669D-28	Sequence 28, Appl
8	96	95.0	118	1 US-08-107-669D-29	Sequence 29, Appl
9	96	95.0	118	1 US-08-107-669D-66	Sequence 66, Appl
10	96	95.0	118	1 US-08-472-788A-28	Sequence 28, Appl
11	96	95.0	118	1 US-08-472-788A-29	Sequence 29, Appl
12	96	95.0	118	1 US-08-472-788A-88	Sequence 88, Appl
13	96	95.0	118	2 US-08-477-531B-28	Sequence 28, Appl
14	96	95.0	118	2 US-08-477-531B-29	Sequence 29, Appl
15	96	95.0	118	2 US-08-477-531B-66	Sequence 66, Appl
16	96	95.0	118	2 US-08-646-360-124	Sequence 124, App
17	96	95.0	118	2 US-08-082-842A-28	Sequence 28, Appl
18	96	95.0	118	2 US-08-082-842A-29	Sequence 29, Appl
19	96	95.0	118	2 US-08-082-842A-88	Sequence 88, Appl
20	96	95.0	118	3 US-08-839-765-124	Sequence 124, App
21	96	95.0	118	3 US-09-136-389-124	Sequence 124, App
22	96	95.0	118	3 US-09-610-838-124	Sequence 124, App
23	96	95.0	118	4 US-09-711-485-124	Sequence 124, App
24	96	95.0	118	4 US-08-569-147-76	Sequence 76, Appl
25	93	92.1	140	3 US-08-569-147-82	Sequence 82, Appl
26	93	92.1	365	3 US-08-875-811-53	Sequence 53, Appl
27	93	92.1	366	3 US-08-875-811-55	Sequence 55, Appl

28	92	91.1	136	3 US-09-184-658-32	Sequence 32, Appl
29	92	91.1	136	4 US-09-504-262D-32	Sequence 32, Appl
30	92	91.1	259	4 US-09-419-788-115	Sequence 115, Appl
31	92	91.1	278	3 US-09-184-658-47	Sequence 47, Appl
32	92	91.1	278	3 US-09-504-262D-47	Sequence 47, Appl
33	92	91.1	284	3 US-09-184-658-40	Sequence 40, Appl
34	92	91.1	284	4 US-09-504-262D-40	Sequence 40, Appl
35	91	90.1	119	4 US-09-232-290-50	Sequence 50, Appl
36	90	89.1	118	1 US-08-425-336-126	Sequence 126, App
37	90	89.1	118	1 US-08-488-113B-126	Sequence 126, App
38	90	89.1	118	1 US-08-477-484B-126	Sequence 126, App
39	90	89.1	118	1 US-08-107-669D-67	Sequence 67, Appl
40	90	89.1	118	1 US-08-472-788A-89	Sequence 89, Appl
41	90	89.1	118	2 US-08-477-531B-67	Sequence 67, Appl
42	90	89.1	118	2 US-08-646-360-126	Sequence 126, App
43	90	89.1	118	2 US-08-082-842A-89	Sequence 89, Appl
44	90	89.1	118	3 US-08-839-765-126	Sequence 126, App
45	90	89.1	118	3 US-09-136-389-126	Sequence 126, App
46	90	89.1	118	3 US-09-610-838-126	Sequence 126, App
47	90	89.1	118	4 US-09-711-485-126	Sequence 126, App
48	90	89.1	240	1 US-08-488-113B-147	Sequence 147, App
49	90	89.1	240	1 US-08-488-113B-148	Sequence 148, App
50	90	89.1	240	1 US-08-477-484B-147	Sequence 147, App
51	90	89.1	240	1 US-08-477-484B-148	Sequence 148, App
52	90	89.1	240	2 US-08-646-360-147	Sequence 147, App
53	90	89.1	240	2 US-08-646-360-148	Sequence 148, App
54	90	89.1	240	3 US-08-839-765-147	Sequence 147, App
55	90	89.1	240	3 US-08-839-765-148	Sequence 148, App
56	90	89.1	240	3 US-09-136-389-147	Sequence 147, App
57	90	89.1	240	3 US-09-136-389-148	Sequence 148, App
58	90	89.1	240	3 US-09-610-838-147	Sequence 147, App
59	90	89.1	240	3 US-09-610-838-148	Sequence 148, App
60	90	89.1	240	4 US-09-711-485-147	Sequence 147, App
61	90	89.1	240	4 US-09-711-485-148	Sequence 148, App
62	89	88.1	230	3 US-09-485-737B-102	Sequence 102, App
63	89	88.1	230	4 US-10-071-485-102	Sequence 102, App
64	89	88.1	235	3 US-09-485-737B-93	Sequence 93, Appl
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66	89	88.1	240	3 US-09-485-737B-91	Sequence 91, Appl
67	89	88.1	240	4 US-10-071-485-91	Sequence 91, Appl
68	89	88.1	267	3 US-09-485-737B-2	Sequence 2, Appl
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71	89	88.1	541	3 US-09-485-737B-85	Sequence 85, Appl
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79	87	86.1	121	4 US-10-011-125A-2	Sequence 2, Appl
80	87	86.1	115	3 US-08-483-749A-24	Sequence 24, Appl
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85	84	83.2	250	2 US-08-356-786-4	Sequence 4, Appl
86	84	83.2	250	1 US-08-133-804-2	Sequence 2, Appl
87	84	83.2	250	1 US-08-461-838-8	Sequence 8, Appl
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90	84	83.2	250	1 US-08-461-838-2	Sequence 2, Appl
91	84	83.2	250	2 US-08-461-838-2	Sequence 2, Appl
92	84	83.2	534	2 US-08-356-786-16	Sequence 16, Appl
93	84	83.2	622	2 US-08-356-786-16	Sequence 16, Appl
94	83	82.2	17	1 US-08-438-123-5	Sequence 5, Appl
95	83	82.2	21	1 US-08-438-123-3	Sequence 3, Appl
96	83	82.2	148	1 US-08-438-123-8	Sequence 8, Appl
97	81	80.2	119	3 US-08-933-983-79	Sequence 79, Appl
98	81	80.2	119	3 US-08-933-983-81	Sequence 81, Appl
99	81	80.2	141	3 US-08-589-939-5	Sequence 5, Appl
100	80	79.2	17	3 US-09-406-532-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1

US-09-318-786-35

Sequence 35, Application US/09318786
Patent No. 6472147
GENERAL INFORMATION:
APPLICANT: Janda, Kim D
APPLICANT: Wirsching, Peter
APPLICANT: Lerner, Richard A
APPLICANT: Gao, Changshou
TITLE OF INVENTION: METHODS FOR DISPLAY OF HETERODIMERIC PROTEINS ON
FILAMENTOUS PHAGE USING PVI1 AND PVI2, COMPOSITIONS,
FILE REFERENCE: T5R03055
CURRENT APPLICATION NUMBER: US/09/318,786
CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 35
LENGTH: 160
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: fusion
US-09-318-786-35

Query Match

Best Local Similarity 97.0%; Score 98; DB 4; Length 160;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYGEPTVADDFKG 17

DB 52 WINTYGEPTVADDFRG 68

RESULT 2

US-08-279-772A-6

Sequence 6, Application US/08279772A
Patent No. 6080560
GENERAL INFORMATION:
APPLICANT: Russell, David R
APPLICANT: Fuller, James T
TITLE OF INVENTION: Method for Producing Antibodies in Plant
TITLE OF INVENTION: Cells
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: Quarles and Brady
STREET: PO Box 2113
CITY: Madison
STATE: WI
COUNTRY: United States of America
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/279,772A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 11-229-9097-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-279-772A-6

Query Match

Best Local Similarity 97.0%; Score 98; DB 3; Length 252;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYGEPTVADDFKG 17

DB 180 WINTYGPFTVADDFKG 196

RESULT 3

US-08-902-486-9

Sequence 9, Application US/08902486
Patent No. 6140075
GENERAL INFORMATION:
APPLICANT: Russell, David R.
APPLICANT: Fuller, James T.
TITLE OF INVENTION: METHOD FOR PRODUCING ANTIBODIES AND
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,486
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 670513.90261
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-902-486-9

Query Match

Best Local Similarity 97.0%; Score 98; DB 3; Length 252;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYGEPTVADDFKG 17

DB 180 WINTYGPFTVADDFKG 196

RESULT 4

US-08-425-336-124

Sequence 124, Application US/08425336
Patent No. 5621083
GENERAL INFORMATION:
APPLICANT: Better, Marc D.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 24, 2005, 08:56:15 ; Search time 98.0156 Seconds
(without alignments)
57.427 Million cell updates/sec

Title: US-10-018-245A-2
Perfect score: 101
Sequence: 1 WINTYGEPTAYADDFKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101	100.0	17	10	US-09-791-551-86
2	101	100.0	17	16	US-10-018-245A-2
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4	101	100.0	70	14	US-10-243-130-17
5	101	100.0	70	14	US-10-243-130-18
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7	101	100.0	70	17	US-10-901-650-18
8	101	100.0	70	17	US-10-901-650-19
9	101	100.0	112	15	US-10-383-447-10
10	101	100.0	112	15	US-10-383-447-18
11	101	100.0	116	14	US-10-138-727A-2
12	101	100.0	116	14	US-10-138-727A-18
13	101	100.0	116	14	US-10-138-727A-19

14	101	100.0	116	14	US-10-138-727A-20	Sequence 20, Appl
15	101	100.0	116	14	US-10-138-727A-21	Sequence 21, Appl
16	101	100.0	116	14	US-10-138-727A-22	Sequence 22, Appl
17	101	100.0	116	14	US-10-138-727A-23	Sequence 23, Appl
18	101	100.0	116	14	US-10-138-727A-24	Sequence 24, Appl
19	101	100.0	116	14	US-10-138-727A-25	Sequence 25, Appl
20	101	100.0	116	14	US-10-138-727A-26	Sequence 26, Appl
21	101	100.0	116	14	US-10-138-727A-27	Sequence 27, Appl
22	101	100.0	116	14	US-10-138-727A-28	Sequence 28, Appl
23	101	100.0	116	14	US-10-138-727A-29	Sequence 29, Appl
24	101	100.0	116	14	US-10-138-727A-30	Sequence 30, Appl
25	101	100.0	116	14	US-10-138-727A-31	Sequence 31, Appl
26	101	100.0	116	14	US-10-138-727A-32	Sequence 32, Appl
27	101	100.0	116	14	US-10-138-727A-33	Sequence 33, Appl
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29	101	100.0	116	14	US-10-138-727A-35	Sequence 35, Appl
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34	101	100.0	116	14	US-10-138-727A-40	Sequence 40, Appl
35	101	100.0	116	14	US-10-138-727A-41	Sequence 41, Appl
36	101	100.0	116	14	US-10-138-727A-42	Sequence 42, Appl
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38	101	100.0	116	14	US-10-138-727A-44	Sequence 44, Appl
39	101	100.0	116	14	US-10-138-727A-45	Sequence 45, Appl
40	101	100.0	117	14	US-10-138-727A-46	Sequence 46, Appl
41	101	100.0	118	14	US-10-138-727A-47	Sequence 47, Appl
42	101	100.0	119	14	US-10-138-727A-48	Sequence 48, Appl
43	101	100.0	119	14	US-10-138-727A-49	Sequence 49, Appl
44	101	100.0	139	14	US-10-138-727A-50	Sequence 50, Appl
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46	101	100.0	579	14	US-10-138-727A-52	Sequence 52, Appl
47	101	100.0	579	14	US-10-138-727A-53	Sequence 53, Appl
48	98	97.0	160	14	US-10-138-727A-54	Sequence 54, Appl
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53	97	96.0	122	15	US-10-138-727A-59	Sequence 59, Appl
54	97	96.0	122	15	US-10-138-727A-60	Sequence 60, Appl
55	97	96.0	469	15	US-10-138-727A-61	Sequence 61, Appl
56	97	96.0	499	15	US-10-138-727A-62	Sequence 62, Appl
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77	93	92.1	253	9	US-10-138-727A-83	Sequence 83, Appl
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79	90	89.1	118	15	US-10-138-727A-85	Sequence 85, Appl
80	90	89.1	118	15	US-10-138-727A-86	Sequence 86, Appl
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83	90	89.1	240	14	US-10-138-727A-89	Sequence 89, Appl
84	90	89.1	240	17	US-10-138-727A-90	Sequence 90, Appl
85	90	89.1	240	17	US-10-138-727A-91	Sequence 91, Appl
86	89	88.1	17	16	US-10-138-727A-92	Sequence 92, Appl

87 89 88.1 123 16 US-10-723-434-106 Sequence 106, App
 88 89 88.1 230 14 US-10-071-485-102 Sequence 102, App
 89 89 88.1 235 14 US-10-071-485-93 Sequence 93, App
 90 89 88.1 240 14 US-10-071-485-91 Sequence 91, App
 91 89 88.1 267 14 US-10-071-485-2 Sequence 2, App
 92 89 88.1 465 15 US-10-404-724-8 Sequence 8, App
 93 89 88.1 465 15 US-10-404-724-23 Sequence 23, App
 94 89 88.1 465 17 US-10-816-276-4 Sequence 4, App
 95 89 88.1 465 17 US-10-816-276-19 Sequence 19, App
 96 89 88.1 468 14 US-10-071-485-67 Sequence 67, App
 97 89 88.1 541 14 US-10-071-485-85 Sequence 85, App
 98 89 88.1 711 14 US-10-071-485-90 Sequence 90, App
 99 88 87.1 116 14 US-10-138-727A-4 Sequence 4, App
 100 88 87.1 116 14 US-10-138-727A-6 Sequence 6, App

ALIGNMENTS

RESULT 1

US-09-791-551-86
 ; Sequence 86, Application US/09791551
 ; Publication No. US20030235584A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KLOETZER, WILLIAM S.
 ; APPLICANT: HANNA, NABIL
 ; TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES
 ; FILE REFERENCE: 037003/0277869
 ; CURRENT APPLICATION NUMBER: US/09/791,551
 ; CURRENT FILING DATE: 2001-02-26
 ; PRIOR APPLICATION NUMBER: 60/185,390
 ; PRIOR FILING DATE: 2000-02-28
 ; PRIOR APPLICATION NUMBER: 60/233,625
 ; PRIOR FILING DATE: 2000-09-18
 ; NUMBER OF SEQ ID NOS: 119
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 86
 ; LENGTH: 17
 ; TYPE: PRT
 ; ORGANISM: Mus sp.
 ; US-09-791-551-86

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 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 WINTYGEPTYADDFKG 17

RESULT 2

US-10-018-245A-2
 ; Sequence 2, Application US/10018245A
 ; Publication No. US20040115196A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FUKUDA, Yoshiaki
 ; APPLICANT: NAGAHARA, Kazuhiro
 ; APPLICANT: MAKASHI, Toshihiro
 ; TITLE OF INVENTION: Novel recombinant antibody, amino acid sequences of its complemer
 ; TITLE OF INVENTION: determining regions and genes encoding the same
 ; FILE REFERENCE: 46224
 ; CURRENT APPLICATION NUMBER: US/10/018,245A
 ; CURRENT FILING DATE: 2002-07-12
 ; PRIOR APPLICATION NUMBER: JP 117394/2000
 ; PRIOR FILING DATE: 2000-04-19
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 17
 ; TYPE: PRT
 ; ORGANISM: mouse
 ; FEATURE:

OTHER INFORMATION: CDR-H2 of anti-human TNF-alpha antibody
 ; US-10-018-245A-2

Query Match 100.0%; Score 101; DB 16; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1,6e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 WINTYGEPTYADDFKG 17

RESULT 3

US-10-243-130-19
 ; Sequence 19, Application US/10243130
 ; Publication No. US20030143682A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nicolaides, Nicholas C.
 ; APPLICANT: Grasso, Luigi M.
 ; APPLICANT: Sasse, Philip M.
 ; TITLE OF INVENTION: ANTIBODIES AND METHODS FOR GENERATING GENETICALLY ALTERED
 ; FILE REFERENCE: MOR-130
 ; CURRENT APPLICATION NUMBER: US/10/243,130
 ; CURRENT FILING DATE: 2002-09-13
 ; PRIOR APPLICATION NUMBER: 09/707,468
 ; PRIOR FILING DATE: 2000-11-07
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 19
 ; LENGTH: 67
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Consensus sequence
 ; US-10-243-130-19

Query Match 100.0%; Score 101; DB 14; Length 67;
 Best Local Similarity 100.0%; Pred. No. 6,4e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WINTYGEPTYADDFKG 17
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 Db 44 WINTYGEPTYADDFKG 60

RESULT 4

US-10-243-130-17
 ; Sequence 17, Application US/10243130
 ; Publication No. US20030143682A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nicolaides, Nicholas C.
 ; APPLICANT: Grasso, Luigi M.
 ; APPLICANT: Sasse, Philip M.
 ; TITLE OF INVENTION: ANTIBODIES AND METHODS FOR GENERATING GENETICALLY ALTERED
 ; TITLE OF INVENTION: ANTIBODIES WITH HIGH AFFINITY
 ; FILE REFERENCE: MOR-130
 ; CURRENT APPLICATION NUMBER: US/10/243,130
 ; CURRENT FILING DATE: 2002-09-13
 ; PRIOR APPLICATION NUMBER: 09/707,468
 ; PRIOR FILING DATE: 2000-11-07
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 17
 ; LENGTH: 70
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-243-130-17

Query Match 100.0%; Score 101; DB 14; Length 70;
 Best Local Similarity 100.0%; Pred. No. 6,7e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Run on: March 24, 2005, 08:54:18 ; Search time 404.547 Seconds
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Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Result Score	Query Match	Length	ID	Description
1	101	100.0	17	US-09-791-551-86	Sequence 86, App1
2	101	100.0	17	US-10-018-245A-2	Sequence 2, App1
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8	101	100.0	19	US-09-191-817-9	Sequence 9, App1
9	101	100.0	19	US-09-191-817-9	Sequence 14, App1
10	101	100.0	19	US-09-831-531A-7	Sequence 7, App1
11	101	100.0	67	PCT-US03-28722-19	Sequence 19, App1
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21	101	100.0	96	US-09-791-537-14482	Sequence 14482, A
22	101	100.0	101	US-09-791-537-83756	Sequence 83756, A
23	101	100.0	105	US-09-791-537-83758	Sequence 83758, A
24	101	100.0	105	US-09-791-537-83758	Sequence 43922, A
25	101	100.0	109	US-09-791-537-82837	Sequence 82837, A
26	101	100.0	110	US-09-791-537-43255	Sequence 43255, A
27	101	100.0	110	US-09-791-537-43255	Sequence 43378, A
28	101	100.0	110	US-09-791-537-43378	Sequence 10, App1
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36	101	100.0	113	PCT-US04-12625-57	Sequence 50, App1
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66	101	100.0	116	US-10-310-719-33	Sequence 33, App1
67	101	100.0	116	US-10-468-370-658	Sequence 658, App
68	101	100.0	116	US-10-468-370-660	Sequence 660, App
69	101	100.0	116	US-10-468-370-662	Sequence 662, App
70	101	100.0	116	US-10-468-370-662	Sequence 662, App

70	101	100.0	116	30	US-10-468-370-664	Sequence 664, App
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83	101	100.0	117	1	PCT-US02-13844A-35	Sequence 35, App1
84	101	100.0	117	6	US-08-292-866-24	Sequence 24, App1
85	101	100.0	117	13	US-08-456-418-20	Sequence 20, App1
86	101	100.0	117	13	US-08-924-754-24	Sequence 24, App1
87	101	100.0	117	13	US-08-924-796-24	Sequence 24, App1
88	101	100.0	117	15	US-09-132-338-24	Sequence 24, App1
89	101	100.0	117	16	US-09-267-281-20	Sequence 20, App1
90	101	100.0	117	22	US-09-791-537-104209	Sequence 104209, App1
91	101	100.0	117	27	US-10-138-727A-35	Sequence 35, App1
92	101	100.0	117	30	US-10-422-049-20	Sequence 20, App1
93	101	100.0	118	6	US-08-292-866-23	Sequence 23, App1
94	101	100.0	118	8	US-08-456-418-19	Sequence 19, App1
95	101	100.0	118	13	US-08-924-754-23	Sequence 23, App1
96	101	100.0	118	13	US-08-924-796-23	Sequence 23, App1
97	101	100.0	118	15	US-09-132-338-23	Sequence 23, App1
98	101	100.0	118	16	US-09-267-281-19	Sequence 19, App1
99	101	100.0	118	22	US-09-791-537-55585	Sequence 55585, App1
100	101	100.0	118	30	US-10-422-049-19	Sequence 19, App1

ALIGNMENTS

RESULT 1
US-09-791-551-86
Sequence 86, Application US/09791551
GENERAL INFORMATION:
APPLICANT: KLOETZER, WILLIAM S.
APPLICANT: HANNA, NABIL
TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES
FILE REFERENCE: 037003/0277869
CURRENT APPLICATION NUMBER: US/09/791,551
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 60/185,390
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: 60/233,625
PRIOR FILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 119
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 86
LENGTH: 17
TYPE: PRT
ORGANISM: Mus sp.
US-09-791-551-86

Query Match 100.0%; Score 101; DB 22; Length 17;
Best Local Similarity 100.0%; Pred. No. 9, 3e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WINTYGEPTYADDFKG 17
Db 1 WINTYGEPTYADDFKG 17

RESULT 2
US-10-018-245A-2
Sequence 2, Application US/10018245A
GENERAL INFORMATION:
APPLICANT: FUKUDA, Yoshiaki
APPLICANT: NAGAHARA, Kazuhito

APPLICANT: NAKANISHI, Toshihiro
TITLE OF INVENTION: Novel recombinant antibody, amino acid sequences of its complement
FILE REFERENCE: 46224
CURRENT APPLICATION NUMBER: US/10/018,245A
CURRENT FILING DATE: 2002-07-12
PRIOR APPLICATION NUMBER: JP 117394/2000
PRIOR FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 17
TYPE: PRT
ORGANISM: mouse
FEATURE:
OTHER INFORMATION: CDR-H2 of anti-human TNF-alpha antibody
US-10-018-245A-2

Query Match 100.0%; Score 101; DB 26; Length 17;
Best Local Similarity 100.0%; Pred. No. 9, 3e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WINTYGEPTYADDFKG 17
Db 1 WINTYGEPTYADDFKG 17

RESULT 3
US-10-672-278-5
Sequence 5, Application US/10672278
GENERAL INFORMATION:
APPLICANT: GOLDBERG, DAVID M.
APPLICANT: HANSEN, HANS J.
APPLICANT: LEUNG, SHUI-ON
TITLE OF INVENTION: CHIMERIC, HUMAN AND HUMANIZED ANTI-GRANULOCYTE
FILE REFERENCE: 40923-0134US1
CURRENT APPLICATION NUMBER: US/10/672,278
CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: PCT/GB03/04229
PRIOR FILING DATE: 2003-09-30
PRIOR APPLICATION NUMBER: 60/414,341
PRIOR FILING DATE: 2002-09-30
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 5
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Chimeric amino
US-10-672-278-5

Query Match 100.0%; Score 101; DB 32; Length 17;
Best Local Similarity 100.0%; Pred. No. 9, 3e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WINTYGEPTYADDFKG 17
Db 1 WINTYGEPTYADDFKG 17

RESULT 4
PCT-US98-24302-14
Sequence 14, Application PC/TUS9824302
GENERAL INFORMATION:
APPLICANT: Purdie Pharma L.P.
TITLE OF INVENTION: IMMUNOGLOBULIN MOLECULES HAVING A SYNTHETIC VARIABLE
FILE REFERENCE: 6750-016-228
CURRENT APPLICATION NUMBER: PCT/US98/24302
CURRENT FILING DATE: 1998-11-13

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:54:17 ; Search time 23.9062 Seconds
(without alignments)
68.421 Million cell updates/sec

Title: US-10-018-245A-2
Perfect score: 101
Sequence: 1 WINTYGEPTVADDFK 17

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	100.0	101	2 D24672	Ig heavy chain V r
2	101	100.0	105	2 S24764	Ig heavy chain V r
3	101	100.0	105	2 S24765	Ig heavy chain V r
4	101	100.0	109	2 S26325	Ig heavy chain V r
5	101	100.0	118	2 S19967	Ig heavy chain V r
6	101	100.0	119	2 A53285	Ig heavy chain V a
7	101	100.0	124	2 PH1404	Ig heavy chain V r
8	98	97.0	115	2 S19968	Ig heavy chain V r
9	98	97.0	120	2 B42848	Ig heavy chain V r
10	98	97.0	146	4 S33905	Ig heavy chain pre
11	97	96.0	102	2 C32530	Ig heavy chain V r
12	92	91.1	105	2 S24766	Ig heavy chain V r
13	91	90.1	118	2 A32530	Ig heavy chain V r
14	90	89.1	114	2 D3267	Ig heavy chain V r
15	90	89.1	114	2 C32967	Ig heavy chain V r
16	90	89.1	117	2 S32187	Ig heavy chain V r
17	90	89.1	117	2 S32190	Ig heavy chain V r
18	89	88.1	136	2 S35759	Ig heavy chain V r
19	88	87.1	119	2 B32530	BHD9D10 protein -
20	86.5	85.6	119	2 H45722	anti-glycoprotein
21	86	85.1	113	2 B36259	Ig heavy chain V r
22	86	85.1	114	2 PL0256	Ig heavy chain V r
23	86	85.1	120	2 S19963	Ig heavy chain V r
24	86	85.1	139	2 PH1225	Ig heavy chain pre
25	84	83.2	93	2 C24672	Ig heavy chain V r
26	84	83.2	99	2 S26326	Ig heavy chain V r
27	83	82.2	115	2 S19965	Ig heavy chain V r
28	78	77.2	118	2 S37204	Ig heavy chain V r
29	75	74.3	120	2 S26789	Ig heavy chain V r

30	73	72.3	98	2 S46460	Ig heavy chain V r
31	73	72.3	105	2 S24763	Ig heavy chain V r
32	68	67.3	98	2 A49051	Ig heavy chain V7
33	68	67.3	117	2 S18554	Ig heavy chain V r
34	68	67.3	131	2 S26792	Ig heavy chain V r
35	64	63.4	142	2 S19245	Ig heavy chain pre
36	63	62.4	98	2 H34964	Ig heavy chain V-I
37	60	59.4	134	2 S21916	Ig heavy chain V r
38	53	52.5	86	2 S54912	Ig heavy chain V r
39	49	48.5	131	2 S21924	Ig heavy chain V r
40	49	48.5	160	2 PL0105	anti-PR2 erythrocy
41	47	46.5	98	2 PH0871	Ig heavy chain V r
42	47	46.5	123	2 D33548	Ig heavy chain V-I
43	46.5	46.0	415	2 AG0301	probable membrane
44	46	45.5	79	2 A49021	Ig heavy chain V-X
45	46	45.5	109	2 PH1668	Ig heavy chain V r
46	46	45.5	127	2 S34014	Ig heavy chain V r
47	46	45.5	470	2 B86165	Ig heavy chain V r
48	45.5	45.0	1020	2 T18260	Ig heavy chain V r
49	45	44.6	98	2 S26912	Ig heavy chain V r
50	45	44.6	98	2 S26938	Ig heavy chain V r
51	45	44.6	98	2 S26919	Ig heavy chain V r
52	45	44.6	111	2 S21925	Ig heavy chain V r
53	45	44.6	114	2 PH1667	Ig heavy chain V r
54	45	44.6	117	2 S31680	Ig heavy chain V r
55	45	44.6	117	2 S18551	Ig heavy chain V r
56	45	44.6	118	2 PH1666	Ig heavy chain V r
57	45	44.6	118	2 S36285	Ig heavy chain V r
58	45	44.6	122	2 S36271	Ig heavy chain V r
59	45	44.6	129	2 S36260	Ig heavy chain V r
60	45	44.6	129	2 S46393	Ig heavy chain V r
61	45	44.6	135	2 S49530	anti-Sm antibody V
62	45	44.6	143	2 AG2289	mutator protein [i
63	45	44.6	1842	2 T43409	probable fatty-acid
64	45	44.6	1842	2 T38781	fatty acid synthase
65	44	43.6	124	2 S19665	Ig heavy chain V r
66	44	43.6	136	1 HVM5B1	Ig heavy chain pre
67	44	43.6	213	2 I40576	hypothetical prote
68	44	43.6	367	2 T26291	hypothetical prote
69	44	43.6	412	2 S30299	Krox-20 protein -
70	44	43.6	446	2 S67437	Damage and replica
71	44	43.6	474	2 S66480	carbon catabolite
72	43.5	43.1	118	2 T09487	hypothetical prote
73	43.5	43.1	145	2 I47185	Ig heavy chain var
74	43	42.6	96	2 S17609	Ig heavy chain V r
75	43	42.6	143	1 E1H0ND	Ig heavy chain pre
76	43	42.6	201	2 A87680	RNA polymerase sig
77	43	42.6	258	2 I64070	cyclase hlsf H1047
78	43	42.6	381	2 AD0191	L-lactate dehydrog
79	43	42.6	434	2 AE3448	guanine deaminase
80	43	42.6	443	2 T21598	hypothetical prote
81	43	42.6	696	2 T02832	long chain fatty a
82	43	42.6	1071	2 T52306	methionine S-methy
83	43	42.6	1951	2 B43963	RNA viral polymera
84	43	42.6	2150	2 S13553	hypothetical prote
85	43	42.6	6486	2 T31076	tyrosidase synthe
86	42.5	42.1	120	1 G1HMD	Ig heavy chain V-I
87	42.5	42.1	264	2 B1362	probable exodeoxyr
88	42.5	42.1	592	2 D70327	glutamine-fructose
89	42	41.6	98	2 S26918	Ig heavy chain V r
90	42	41.6	98	2 S17604	Ig heavy chain V r
91	42	41.6	110	2 PH1670	Ig heavy chain V r
92	42	41.6	114	2 S26319	Ig heavy chain V r
93	42	41.6	117	2 S18553	Ig heavy chain V r
94	42	41.6	118	2 S25174	Ig heavy chain V r
95	42	41.6	118	2 F72529	hypothetical prote
96	42	41.6	132	2 S31596	Ig heavy chain V r
97	42	41.6	135	2 PS0057	Ig heavy chain pre
98	42	41.6	136	2 S31600	Ig heavy chain V r
99	42	41.6	136	2 S04576	Ig heavy chain pre
100	42	41.6	155	2 T13308	hypothetical prote

ALIGNMENTS

RESULT 1

D24672

Ig heavy chain V region (VGM3-8) - mouse (fragment)
C/Species: Mus musculus (house mouse)

C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999

C/Accession: D24672

R/Winter, B.; Radbruch, A.; Krawinkel, U.

EMBO J. 4, 2861-2867, 1985

A/Reference number: A91022; MUID:86055722; PMID:2998759

A/Accession: D24672

A/Molecule type: DNA

A/Residues: 1-101 <WIN>

A/Cross-references: GB:X03301; NID:g51757; PIDN:CAA27040.1; PID:g773215

A/Note: this sequence was determined from the differentiated gene

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 101; DB 2; Length 101;

Best Local Similarity 100.0%; Pred. No. 1e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYTGEPYADDFKG 17

Db 31 WINTYTGEPYADDFKG 47

RESULT 2

S24764

Ig heavy chain V region (subgroup XI) - mouse (fragment)
C/Species: Mus musculus (house mouse)

C/Date: 20-Feb-1995 #sequence_revision 21-Nov-1998 #text_change 23-Jul-1999

C/Accession: S24764; S24772; S24777

R/Klages, S.

submitted to the EMBL Data Library, August 1992

A/Reference number: S24763

A/Accession: S24764

A/Molecule type: DNA

A/Residues: 1-105 <KLA>

A/Accession: S24772

A/Molecule type: DNA

A/Residues: 1-105 <KLM>

A/Cross-references: EMBL:Z15011

R/Thomas, J.W.

submitted to the EMBL Data Library, August 1992

A/Reference number: S24776

A/Accession: S24777

A/Molecule type: DNA

A/Residues: 1-105 <THO>

A/Cross-references: EMBL:Z15020; NID:g52616; PIDN:CAA78739.1; PID:g52617

C/Genetics: 9/1

A/Intons: 9/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 101; DB 2; Length 105;

Best Local Similarity 100.0%; Pred. No. 1.1e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYTGEPYADDFKG 17

Db 62 WINTYTGEPYADDFKG 78

RESULT 3

S24765

Ig heavy chain V region (subgroup XI) - mouse (fragment)
C/Species: Mus musculus (house mouse)

C/Date: 20-Feb-1995 #sequence_revision 21-Nov-1998 #text_change 23-Jul-1999

C/Accession: S24765; S24773; S24778

R/Klages, S.

submitted to the EMBL Data Library, August 1992

A/Reference number: S24763

A/Accession: S24765

A/Molecule type: DNA

A/Residues: 1-105 <KLA>

A/Cross-references: EMBL:Z15001

A/Accession: S24773

A/Molecule type: DNA

A/Residues: 1-105 <KLM>

A/Cross-references: EMBL:Z15013

R/Thomas, J.W.

submitted to the EMBL Data Library, August 1992

A/Reference number: S24776

A/Accession: S24778

A/Molecule type: DNA

A/Residues: 1-105 <THO>

A/Cross-references: EMBL:Z15022; NID:g52619; PIDN:CAA78741.1; PID:g52620

C/Genetics: 9/1

A/Intons: 9/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 101; DB 2; Length 105;

Best Local Similarity 100.0%; Pred. No. 1.1e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYTGEPYADDFKG 17

Db 62 WINTYTGEPYADDFKG 78

RESULT 4

S26325

Ig heavy chain V region - mouse
C/Species: Mus musculus (house mouse)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C/Accession: S26325

R/Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A/Title: Antibodies that are specific for a single amino acid interchange in a protein ei

A/Reference number: S26309; MUID:91341421; PMID:1908510

A/Accession: S26325

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-109 <STA>

A/Cross-references: UNIPROT:Q921A6; EMBL:X59210; NID:g52080; PID:g1334043

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;5-88/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 101; DB 2; Length 109;

Best Local Similarity 100.0%; Pred. No. 1.1e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WINTYTGEPYADDFKG 17

Db 40 WINTYTGEPYADDFKG 56

RESULT 5

S19967

Ig heavy chain V region (M-T406) - mouse (fragment)
C/Species: Mus musculus (house mouse)

C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004

C/Accession: S19967

R/Weissenhorn, W.; Riethmüller, G.; Weiss, E.M.; Rieber, E.P.

submitted to the EMBL Data Library, March 1992

A/Description: Structural characterization of CD4 mAb.

A/Reference number: S19963

A/Accession: S19967

A/Status: preliminary

A/Molecule type: mRNA

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:54:17 ; Search time 112.094 Seconds
(without alignments)
77.661 Million cell updates/sec

Title: US-10-018-245A-2
Perfect score: 101
Sequence: 1 WINTYTGEPYADDFK 17

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	100.0	241	2	Q921A6
2	92	91.1	102	2	Q91L79
3	87	86.1	116	2	Q683Y7
4	87	86.1	116	2	Q683Y8
5	86	85.1	140	2	Q652L3
6	73	72.3	125	2	Q6P1L0
7	72	71.3	484	2	Q99LA6
8	71	70.3	218	2	Q925S1
9	51	50.5	381	2	Q9GNT8
10	50	49.5	379	2	Q87G18
11	49	48.5	610	2	Q9HKR6
12	49	48.5	1549	2	Q76D19
13	48	47.5	500	2	Q6N091
14	48	47.5	2009	2	Q7N848
15	48	47.5	2151	2	Q6B7Y9
16	48	47.5	2992	2	Q7RXD7
17	47	46.5	518	2	Q6N030
18	47	46.5	1085	2	Q852S0
19	46.5	46.0	414	2	Q669H4
20	46.5	46.0	415	2	Q8ZDP6
21	46	45.5	154	2	Q6UP30
22	46	45.5	341	2	Q8ZWT8
23	46	45.5	470	2	Q9ZVT6
24	45.5	45.0	244	2	Q6MX64
25	45.5	45.0	1020	1	VP34 CANAL
26	45	44.6	143	2	Q8YOG1
27	45	44.6	182	2	Q8G4B6
28	45	44.6	389	2	Q752V2
29	45	44.6	411	2	Q6PPG2
30	45	44.6	469	2	Q7Z7P5
31	45	44.6	487	2	Q6QBS6

32	45	44.6	507	2	P955S2	P955S2 pseudomonas
33	45	44.6	527	2	Q65FV7	Q65FV7 bacillus 11
34	45	44.6	576	2	Q65WZ7	Q65WZ7 oryza sativ
35	45	44.6	745	2	Q6LZ19	Q6LZ19 methanococ
36	45	44.6	753	2	Q9EY04	Q9EY04 clostridium
37	45	44.6	759	2	Q8A3F1	Q8A3F1 bacteroides
38	45	44.6	868	2	Q8A2M9	Q8A2M9 bacteroides
39	45	44.6	1842	1	FAS2_SCHPO	Q10289 s fatty aci
40	44.5	44.1	191	2	Q9NUY2	Q9NUY2 giardia lam
41	44.5	44.1	469	2	Q7XU9	Q7XU9 allium cepa
42	44	43.6	136	1	HV15_MOUSE	P01759 mus musculu
43	44	43.6	213	2	Q45776	Q45776 bacteroides
44	44	43.6	213	2	Q72AR7	Q72AR7 desulfovibr
45	44	43.6	215	2	Q81HL9	Q81HL9 trossophila
46	44	43.6	220	2	Q830L3	Q830L3 enterococcu
47	44	43.6	310	2	Q9APR2	Q9APR2 oryza sativ
48	44	43.6	353	2	Q8L0J3	Q8L0J3 uncultured
49	44	43.6	366	2	Q8V091	Q8V091 uncultured
50	44	43.6	367	2	Q7YTW2	Q7YTW2 caenorhabdi
51	44	43.6	394	2	Q89YX4	Q89YX4 bacteroides
52	44	43.6	402	2	Q7VX60	Q7VX60 bordetella
53	44	43.6	402	2	Q7W826	Q7W826 bordetella
54	44	43.6	402	2	Q7WLH3	Q7WLH3 bordetella
55	44	43.6	411	2	Q68A45	Q68A45 ralsictonia s
56	44	43.6	412	1	EG2B_BRARE	Q05159 brachydantio
57	44	43.6	412	2	Q66HT5	Q66HT5 brachydantio
58	44	43.6	416	2	Q8XR46	Q8XR46 ralsictonia s
59	44	43.6	446	1	CRB3_SCHPO	Q10272 schizosacch
60	44	43.6	462	2	Q98T82	Q98T82 galius galli
61	44	43.6	474	1	MIG1_KLUTA	P50898 kluyveromyc
62	44	43.6	497	2	Q8WY24	Q8WY24 homo sapien
63	44	43.6	543	1	MIG1_KLUMA	P52288 kluyveromyc
64	44	43.6	739	2	Q8LVD0	Q8LVD0 foot-and-mo
65	44	43.6	771	2	Q9XHY4	Q9XHY4 oryza sativ
66	43.5	43.1	118	2	Q48377	Q48377 bacteriopho
67	43.5	43.1	118	2	Q71TD1	Q71TD1 bacteriopho
68	43.5	43.1	424	2	Q6D859	Q6D859 erwinia car
69	43	42.6	120	2	Q606D1	Q606D1 ixodes ricci
70	43	42.6	133	2	Q836K9	Q836K9 enterococcu
71	43	42.6	147	1	HV1C_HUMAN	P01744 homo sapien
72	43	42.6	201	2	Q9A2T1	Q9A2T1 caulobacter
73	43	42.6	202	2	Q95W67	Q95W67 myxine glut
74	43	42.6	258	1	HIS6_HAEIN	P44436 haemophilus
75	43	42.6	264	2	Q6FFG3	Q6FFG3 actinobact
76	43	42.6	352	2	Q8KZU4	Q8KZU4 uncultured
77	43	42.6	352	2	Q6LOC2	Q6LOC2 uncultured
78	43	42.6	381	2	Q66C32	Q66C32 yersinia ps
79	43	42.6	381	2	Q8ZFW8	Q8ZFW8 yersinia ps
80	43	42.6	434	2	Q8YFPI	Q8YFPI bruceella me
81	43	42.6	436	2	Q8G2G8	Q8G2G8 bruceella su
82	43	42.6	436	1	Y96X_RHIL0	Q98P28 rhizobium l
83	43	42.6	453	2	Q8ZFT6	Q8ZFT6 streptomyce
84	43	42.6	537	2	Q9L6J3	Q9L6J3 oryza sativ
85	43	42.6	572	2	Q454Z2	Q454Z2 caenorhabdi
86	43	42.6	573	2	Q8A3Y7	Q8A3Y7 bacteroides
87	43	42.6	696	2	Q15838	Q15838 leishmania
88	43	42.6	763	1	THED_CONGL	Q8NQH1 c multifunc
89	43	42.6	879	2	Q6BIR4	Q6BIR4 debaryomyc
90	43	42.6	938	2	Q8K0N8	Q8K0N8 mus musculu
91	43	42.6	1071	1	MMT1_ARATH	Q1162 arabisidopsi
92	43	42.6	1282	1	BMS1_HUMAN	Q14692 homo sapien
93	43	42.6	1284	2	Q6PGF5	Q6PGF5 mus musculu
94	43	42.6	1287	2	Q6ZOH0	Q6ZOH0 mus musculu
95	43	42.6	151	1	RKPL_HANTV	P23456 hantaa vir
96	43	42.6	2151	2	Q99AT5	Q99AT5 hantaa vir
97	43	42.6	2151	2	Q89913	Q89913 hantaa vir
98	43	42.6	2151	2	Q9DVX9	Q9DVX9 hantavirus
99	43	42.6	2151	2	Q9E127	Q9E127 hantavirus
100	43	42.6	2151	2	Q9QD48	Q9QD48 hantavirus

ALIGNMENTS

```

RESULT 1
Q921A6 PRELIMINARY; PRT; 241 AA.
ID 0921A6
AC 0921A6
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Anti-CEA 79 single chain Fv (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Y1 K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scFv).";
RL Mol. Cells 7:816-819 (1997).
DR EMBL: U88067; AAB48044.1; -.
DR PIR: S19965; S19965.
DR PIR: S19967; S19967.
DR PIR: S19968; S19968.
DR PIR: S26325; S26325.
DR HSSP: P01607; 1BMW.
DR SMART: SM00406; IGV; 2.
DR PROSITE: PS50835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 241
SQ SEQUENCE 241 AA; 26086 MW; 02768872489C771 CRC64;

Query Match 100.0%; Score 101; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 2,1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WINTYGEPTVADDFKG 17
Db 50 WINTYGEPTVADDFKG 66

RESULT 2
Q9JL79 PRELIMINARY; PRT; 102 AA.
ID 09JL79
AC 09JL79
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A.CA;
RX MEDLINE=20448942; PubMed=10992488;
RX DOI=10.1128/IAI.68.10.5803-5808.2000;
RA Malik S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin";
RL Infect. Immun. 68:5803-5808 (2000).
DR EMBL: AF206027; AAF69325.1; -.
DR HSSP: P01751; 1NOB.
DR InterPro: IPR007110; IG_1-like.
DR InterPro: IPR003596; IGV.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 102
SQ SEQUENCE 102 AA; 12863 MW; 5EC1AD02E911952 CRC64;

Query Match 86.1%; Score 87; DB 2; Length 116;
Best Local Similarity 88.2%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WINTYGEPTVADDFKG 17
Db 50 WINTYGEPTVADDFKG 66

RESULT 4
Q683Y8 PRELIMINARY; PRT; 116 AA.
ID 0683Y8
AC 0683Y8
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Immunoglobulin heavy chain variable region (Fragment).
GN Name=IGHV;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Balb/c;
RA Phalipon A., Costachel C., Thuniz A., Nato F.;
RT "Anti-lipoplysaccharide antibodies protective against Shigella
RT flexneri 2a infection recognize an immunodominant serotype-specific

```

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FT NON_TER 102
SQ SEQUENCE 102 AA; 11543 MW; E590C292093F6711 CRC64;

Query Match 91.1%; Score 92; DB 2; Length 102;
Best Local Similarity 94.1%; Pred. No. 2,6e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WINTYGEPTVADDFKG 17
Db 35 WINTYGEPTVADDFKG 51

RESULT 3
Q683Y7 PRELIMINARY; PRT; 116 AA.
ID 0683Y7
AC 0683Y7
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Immunoglobulin heavy chain variable region (Fragment).
GN Name=IGHV;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Balb/c;
RA Phalipon A., Costachel C., Thuniz A., Nato F.;
RT "Anti-lipoplysaccharide antibodies protective against Shigella
RT flexneri 2a infection recognize an immunodominant serotype-specific
RT determinant on the O-antigen.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ784033; CAH04483.1; -.
DR InterPro: IPR003599; IGV.
DR InterPro: IPR007110; IG_1-like.
DR InterPro: IPR003596; IGV.
DR PIR: PFO0047; IGV; 1.
DR SMART: SM00409; IGV; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12863 MW; 5EC1AD02E911952 CRC64;

Query Match 86.1%; Score 87; DB 2; Length 116;
Best Local Similarity 88.2%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WINTYGEPTVADDFKG 17
Db 50 WINTYGEPTVADDFKG 66

RESULT 4
Q683Y8 PRELIMINARY; PRT; 116 AA.
ID 0683Y8
AC 0683Y8
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Immunoglobulin heavy chain variable region (Fragment).
GN Name=IGHV;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Balb/c;
RA Phalipon A., Costachel C., Thuniz A., Nato F.;
RT "Anti-lipoplysaccharide antibodies protective against Shigella
RT flexneri 2a infection recognize an immunodominant serotype-specific

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:54:17 ; Search time 60.75 Seconds
(without alignments)
50.931 Million cell updates/sec

Title: US-10-018-245A-3
Perfect score: 51
Sequence: 1 YDYDGFDPY 8

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseq1980s:*
2: geneseq1990s:*
3: geneseq2000s:*
4: geneseq2001s:*
5: geneseq2002s:*
6: geneseq2003as:*
7: geneseq2003bs:*
8: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	8	5	AAG80313
2	51	100.0	117	5	AAG80317
3	44	86.3	108	6	ABU02662
4	44	86.3	108	8	ADK47752
5	44	86.3	120	8	ADR94312
6	43	84.3	120	2	AAW05825
7	43	84.3	139	2	AAW36167
8	43	84.3	139	2	AAW36165
9	43	84.3	182	6	ABU70516
10	43	84.3	279	2	AAW05826
11	43	84.3	359	4	AAE04200
12	43	84.3	359	8	ABG64502
13	43	84.3	359	8	ADL77769
14	43	84.3	363	3	AAW36391
15	43	84.3	408	5	ABP69127
16	43	84.3	542	3	AAW36394
17	43	84.3	592	4	AAE04244
18	43	84.3	706	5	ABP69128
19	43	84.3	708	3	AAU09860
20	43	84.3	736	3	AAW36392
21	43	84.3	736	4	AAW36392
22	43	84.3	736	4	AAW36392
23	43	84.3	736	4	AAW36392
24	43	84.3	736	4	AAW36392
25	43	84.3	736	4	AAW36392

26	43	84.3	736	5	ADI28041
27	43	84.3	747	3	AAW36393
28	43	84.3	747	7	ABR63160
29	43	84.3	804	4	AAW94482
30	43	84.3	806	5	ABG66709
31	43	84.3	806	5	ABG66686
32	42	82.4	144	2	AAW08346
33	40.5	79.4	11	8	ADSI18692
34	40.5	79.4	11	8	ADSI18692
35	40.5	79.4	450	8	ADSI18702
36	40.5	79.4	450	8	ADSI18702
37	40	78.4	12	2	AAW27040
38	40	78.4	121	2	AAW53584
39	40	78.4	121	5	ABG32687
40	40	78.4	121	5	ABG32695
41	40	78.4	121	5	ABG32683
42	40	78.4	121	5	ABG32693
43	40	78.4	121	5	ABG32689
44	40	78.4	121	5	ABG32685
45	40	78.4	121	5	ABG32681
46	40	78.4	121	5	ABG32691
47	40	78.4	121	5	AAE27809
48	40	78.4	121	5	AAE27823
49	40	78.4	121	5	AAE27815
50	40	78.4	121	5	AAE27821
51	40	78.4	121	5	AAE27811
52	40	78.4	121	5	AAE27813
53	40	78.4	121	5	AAE27817
54	40	78.4	121	5	AAE27819
55	40	78.4	140	2	AAW27049
56	40	78.4	140	2	AAW27051
57	40	78.4	242	2	AAW79870
58	40	78.4	242	2	AAW79872
59	40	78.4	242	2	AAW79871
60	40	78.4	244	2	AAW79868
61	40	78.4	244	2	AAW79867
62	40	78.4	244	2	AAW79873
63	40	78.4	246	2	AAW79869
64	40	78.4	574	6	ABP72635
65	40	78.4	652	2	AAW48650
66	39	76.5	120	4	AAW13721
67	39	76.5	124	4	AAW13825
68	39	76.5	124	4	AAW32770
69	39	76.5	124	4	AAW26232
70	39	76.5	124	4	ABW12600
71	39	76.5	124	4	ABW12600
72	39	76.5	124	4	ABW12600
73	39	76.5	124	4	AAW65958
74	39	76.5	124	4	AAW65958
75	39	76.5	124	4	ABG47622
76	39	76.5	124	4	AAW01569
77	39	76.5	124	4	ABG35604
78	39	76.5	161	5	ABW77790
79	39	76.5	515	8	ADW66025
80	39	76.5	515	8	ADW66025
81	39	76.5	545	2	AAW24418
82	39	76.5	545	2	AAW24418
83	39	76.5	561	5	ABW77791
84	39	76.5	561	7	ABW77791
85	39	76.5	561	7	ABW77791
86	39	76.5	561	7	ABW77791
87	39	76.5	561	7	ABW77791
88	39	76.5	561	7	ABW77791
89	39	76.5	561	7	ABW77791
90	39	76.5	561	7	ABW77791
91	39	76.5	561	7	ABW77791
92	39	76.5	561	7	ABW77791
93	39	76.5	561	7	ABW77791
94	39	76.5	561	7	ABW77791
95	39	76.5	561	7	ABW77791
96	39	76.5	561	7	ABW77791
97	39	76.5	561	7	ABW77791
98	39	76.5	561	7	ABW77791

99 38 74.5 105 3 AAY77993
100 38 74.5 119 2 AAR25728

AAY77993 Amino aci
AAR25728 Humanised

ALIGNMENTS

RESULT 1
AAG80313 standard; peptide; 8 AA.

XX AAG80313;

XX 18-FEB-2002 (first entry)

XX Anti-human TNF-alpha CDR-H3 peptide.

XX TNF-alpha; tumour necrosis factor-alpha; antibody; anti-human; CDR;
KM heavy chain; light chain; complementarity determining region; vasotrophic;
KM antiarthritic; neuroprotective; protozoacide; toxic shock syndrome;
KM rheumatoid arthritis; malaria; multiple sclerosis.

XX Homo sapiens.

XX MO200179298-A1.

XX 25-OCT-2001.

XX 18-APR-2001; 2001WO-JP003308.

XX 19-APR-2000; 2000JP-00117394.

XX (SUNR) SUNTORY LTD.

XX Fukuda Y, Nagahira K, Nakanishi T;

XX WPI; 2002-066345/09.

XX Novel heavy and light-chain polypeptides of chimeric and humanized
PT antibodies against human tumor necrosis factor alpha for low-
PT immunogenicity treatment of TNF-related diseases such as toxic shock
PT syndrome.

XX Claim 1c; Page 26; 36pp; Japanese.

XX This invention describes novel heavy chain and light chain polypeptides
CC or their fragments of a recombinant antibody to human TNF-alpha which
CC contain complementarity determining region (CDR) sequences. The products
CC of the invention have vasotrophic, antiarthritic, neuroprotective and
CC vivo. The antibodies act by neutralising TNF-alpha in
CC associated diseases such as toxic shock syndrome, rheumatoid arthritis,
CC malaria and multiple sclerosis. The antibodies have low immunogenicity in
CC humans. This sequence represents the anti-human tumour necrosis factor-
CC alpha (TNF-alpha) heavy chain CDR1 designated CDR-H3

XX Sequence 8 AA;

Query Match 100.0%; Score 51; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YDYDGFY 8
|||
Db 1 YDYDGFY 8

RESULT 2
AAG80317 standard; protein; 117 AA.
XX AAG80317;
AC AAG80317;

XX 18-FEB-2002 (first entry)

XX Anti-human TNF-alpha H chain CDR region.

XX TNF-alpha; tumour necrosis factor-alpha; antibody; anti-human; CDR;
KM heavy chain; light chain; complementarity determining region; vasotrophic;
KM antiarthritic; neuroprotective; protozoacide; toxic shock syndrome;
KM rheumatoid arthritis; malaria; multiple sclerosis.

XX Homo sapiens.

XX MO200179298-A1.

XX 25-OCT-2001.

XX 18-APR-2001; 2001WO-JP003308.

XX 19-APR-2000; 2000JP-00117394.

XX (SUNR) SUNTORY LTD.

XX Fukuda Y, Nagahira K, Nakanishi T;

XX WPI; 2002-066345/09.

XX N-PSDB; AAI69375.

XX Novel heavy and light-chain polypeptides of chimeric and humanized
PT antibodies against human tumor necrosis factor alpha for low-
PT immunogenicity treatment of TNF-related diseases such as toxic shock
PT syndrome.

XX Disclosure; Page 27-28; 36pp; Japanese.

XX This invention describes novel heavy chain and light chain polypeptides
CC or their fragments of a recombinant antibody to human TNF-alpha which
CC contain complementarity determining region (CDR) sequences. The products
CC of the invention have vasotrophic, antiarthritic, neuroprotective and
CC vivo. The antibodies act by neutralising TNF-alpha in
CC associated diseases such as toxic shock syndrome, rheumatoid arthritis,
CC malaria and multiple sclerosis. The antibodies have low immunogenicity in
CC humans. This sequence represents the anti-human tumour necrosis factor-
CC alpha (TNF-alpha) heavy chain CDR fragment described in the invention

XX Sequence 117 AA;

Query Match 100.0%; Score 51; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.8; 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YDYDGFY 8
|||
Db 99 YDYDGFY 106

RESULT 3
ABU02662

ID ABU02662 standard; protein; 108 AA.

XX ABU02662;

XX 23-OCT-2003 (revised)

XX 11-FEB-2003 (first entry)

XX S. pneumoniae type 4 strain protein from coding region #2241.

XX Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection;
KM antiinflammatory; antibacterial; immunostimulant; auditory; respiratory;
KM gene therapy; vaccine.

XX Streptococcus pneumoniae; type 4 strain.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:57:11 ; Search time 16.125 Seconds
(without alignments)
37.035 Million cell updates/sec

Title: US-10-018-245A-3
Perfect score: 51
Sequence: 1 YDYDGFDPY 8

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	86.3	108	4	US-09-583-110-4267
2	44	86.3	120	4	US-09-107-433-2947
3	44	84.3	120	3	US-08-397-411-10
4	43	84.3	120	3	US-08-397-411-11
5	43	84.3	139	2	US-08-656-586-4
6	43	84.3	139	2	US-08-656-586-8
7	43	84.3	279	3	US-08-397-411-13
8	40	78.4	12	1	US-07-946-421-6
9	40	78.4	121	4	US-09-254-180C-7
10	40	78.4	140	1	US-07-946-421-24
11	40	78.4	140	1	US-07-946-421-28
12	40	78.4	242	2	US-08-553-497A-26
13	40	78.4	242	2	US-08-553-497A-28
14	40	78.4	244	2	US-08-553-497A-20
15	40	78.4	244	2	US-08-553-497A-22
16	40	78.4	246	2	US-08-553-497A-24
17	39	76.5	161	4	US-09-821-687-2
18	39	76.5	545	2	US-08-990-114-1
19	39	76.5	545	3	US-09-241-333-1
20	39	76.5	561	4	US-09-821-687-4
21	38	74.5	119	1	US-07-634-278-37
22	38	74.5	119	1	US-07-634-278-60
23	38	74.5	119	1	US-07-634-278-61
24	38	74.5	119	1	US-08-477-728-37
25	38	74.5	119	1	US-08-477-728-60
26	38	74.5	119	1	US-08-477-728-61
27	38	74.5	119	1	US-08-474-040-37

28	38	74.5	119	1	US-08-474-040-60	Sequence 60, Appl
29	38	74.5	119	1	US-08-474-040-61	Sequence 61, Appl
30	38	74.5	119	1	US-08-487-200-37	Sequence 37, Appl
31	38	74.5	119	1	US-08-487-200-60	Sequence 60, Appl
32	38	74.5	119	1	US-08-487-200-61	Sequence 61, Appl
33	38	74.5	119	1	US-08-484-537-37	Sequence 37, Appl
34	38	74.5	119	3	US-08-484-537-60	Sequence 60, Appl
35	38	74.5	119	3	US-08-484-537-61	Sequence 61, Appl
36	38	74.5	138	1	US-07-634-278-33	Sequence 33, Appl
37	38	74.5	138	1	US-08-477-728-33	Sequence 33, Appl
38	38	74.5	138	1	US-08-474-040-33	Sequence 33, Appl
39	38	74.5	138	1	US-08-487-200-33	Sequence 33, Appl
40	38	74.5	138	3	US-08-484-537-33	Sequence 33, Appl
41	38	74.5	329	4	US-09-270-767-46040	Sequence 46040, A
42	37	72.5	10	1	US-08-318-9708-8	Sequence 8, Appl
43	37	72.5	363	4	US-09-489-039A-7321	Sequence 7321, Ap
44	37	72.5	654	1	US-08-332-828C-2	Sequence 2, Appl
45	37	72.5	654	3	US-09-330-945-2	Sequence 2, Appl
46	37	72.5	697	4	US-09-248-796A-15295	Sequence 15295, A
47	36	70.6	63	4	US-09-248-796A-21570	Sequence 21570, A
48	36	70.6	116	2	US-08-308-494A-21	Sequence 21, Appl
49	36	70.6	236	1	US-08-335-695-22	Sequence 22, Appl
50	36	70.6	257	4	US-09-338-092-18	Sequence 18, Appl
51	36	70.6	319	4	US-09-710-279-2760	Sequence 2760, Ap
52	36	70.6	443	3	US-09-134-001C-3183	Sequence 3183, Ap
53	36	70.6	571	4	US-09-543-681A-4700	Sequence 4700, Ap
54	36	70.6	607	4	US-09-570-856B-28	Sequence 28, Appl
55	36	70.6	728	4	US-09-543-681A-8132	Sequence 8132, Ap
56	35	68.6	70	4	US-09-107-532A-5874	Sequence 5874, Ap
57	35	68.6	114	4	US-09-248-796A-27842	Sequence 27842, A
58	35	68.6	260	4	US-09-270-767-43301	Sequence 43301, A
59	35	68.6	289	4	US-09-949-016-8825	Sequence 8825, Ap
60	35	68.6	341	4	US-09-107-532A-3743	Sequence 3743, Ap
61	35	68.6	350	2	US-08-484-905-65	Sequence 65, Appl
62	35	68.6	350	2	US-08-484-905-67	Sequence 67, Appl
63	35	68.6	350	3	US-08-481-985B-65	Sequence 65, Appl
64	35	68.6	350	3	US-08-481-985B-67	Sequence 67, Appl
65	35	68.6	350	3	US-08-370-476-65	Sequence 65, Appl
66	35	68.6	350	3	US-08-370-476-67	Sequence 67, Appl
67	35	68.6	361	3	US-08-652-265-22	Sequence 22, Appl
68	35	68.6	361	3	US-08-834-497A-22	Sequence 22, Appl
69	35	68.6	361	3	US-09-503-444A-22	Sequence 22, Appl
70	35	68.6	531	4	US-09-248-796A-20235	Sequence 20235, A
71	35	68.6	1060	4	US-09-419-768-19	Sequence 19, Appl
72	34.5	67.6	119	1	US-08-491-845-2	Sequence 2, Appl
73	34.5	67.6	119	1	US-08-491-845-10	Sequence 10, Appl
74	34	66.7	14	4	US-08-914-372C-16	Sequence 16, Appl
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76	34	66.7	20	2	US-08-488-379-207	Sequence 207, App
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78	34	66.7	20	4	US-08-077-255A-207	Sequence 207, App
79	34	66.7	20	5	PCT-US93-07545-207	Sequence 207, App
80	34	66.7	58	3	US-08-812-586-5	Sequence 5, Appl
81	34	66.7	58	3	US-09-535-832A-5	Sequence 5, Appl
82	34	66.7	61	4	US-09-270-767-38509	Sequence 38509, A
83	34	66.7	61	4	US-09-270-767-53726	Sequence 53726, A
84	34	66.7	92	4	US-09-673-809-106	Sequence 106, App
85	34	66.7	105	3	US-08-812-586-1	Sequence 1, Appl
86	34	66.7	105	4	US-09-535-832A-1	Sequence 1, Appl
87	34	66.7	156	4	US-09-513-999C-4289	Sequence 4289, Ap
88	34	66.7	182	1	US-08-137-954-135	Sequence 135, App
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90	34	66.7	182	1	US-08-137-954-138	Sequence 138, App
91	34	66.7	182	1	US-08-137-954-139	Sequence 139, App
92	34	66.7	182	1	US-08-137-954-140	Sequence 140, App
93	34	66.7	182	1	US-08-137-954-141	Sequence 141, App
94	34	66.7	182	1	US-08-137-954-142	Sequence 142, App
95	34	66.7	182	1	US-08-137-954-143	Sequence 143, App
96	34	66.7	182	1	US-08-137-954-144	Sequence 144, App
97	34	66.7	182	1	US-08-137-954-145	Sequence 145, App
98	34	66.7	182	1	US-08-127-954-150	Sequence 150, App
99	34	66.7	182	1	US-08-127-954-151	Sequence 151, App
100	34	66.7	182	1	US-08-127-954-152	Sequence 152, App

ALIGNMENTS

RESULT 1
US-09-583-110-4267
Sequence 4267, Application US/09583110
Patent No. 6699703
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATH00-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 4267
LENGTH: 108
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-583-110-4267

Query Match 86.3%; Score 44; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYDGFY 8
Db 99 DYDGFY 105

RESULT 2
US-09-107-433-2947
Sequence 2947, Application US/09107433
Patent No. 6800744
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESSES:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Denise
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:

TELEPHONE: (781) 893-5007
TELEFAX: (781) 893-8277
INFORMATION FOR SEQ ID NO: 2947:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
MOLECULE TYPE: linear
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
FEATURE:
NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1..120
SEQUENCE DESCRIPTION: SEQ ID NO: 2947:
US-09-107-433-2947

Query Match 86.3%; Score 44; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYDGFY 8
Db 111 DYDGFY 117

RESULT 3
US-08-397-411-10
Sequence 10, Application US/08397411
Patent No. 6129914
GENERAL INFORMATION:
APPLICANT: Weiner, George
APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
APPLICANT: Teo, J. Yun
TITLE OF INVENTION: Bispecific Antibody Effective to Treat
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,411
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-004901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-397-411-10

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OM protein - protein search, using sw model

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Title: US-10-018-245A-3

Perfect score: 51

Sequence: 1 YDYDGFDPY 8

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Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 100 summaries

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20: /cgn2_6/ptodata/2/pubppaa/US60_PUBSCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	43	84.3	120	15	US-10-435-299-11
5	43	84.3	279	15	US-10-435-299-13
6	43	84.3	359	11	US-09-833-245-1251
7	43	84.3	363	13	US-10-045-815-2
8	43	84.3	446	17	US-10-822-300-136
9	43	84.3	446	17	US-10-822-300-137
10	43	84.3	446	17	US-10-822-300-138
11	43	84.3	446	17	US-10-822-300-139
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13	43	84.3	542	13	US-10-045-815-8

14	43	84.3	708	15	US-10-257-174-25	Sequence 25, Appl
15	43	84.3	736	13	US-10-045-815-4	Sequence 4, Appl
16	43	84.3	736	15	US-10-257-174-26	Sequence 26, Appl
17	43	84.3	736	15	US-10-312-352-33	Sequence 33, Appl
18	43	84.3	747	13	US-10-045-815-6	Sequence 6, Appl
19	40	78.4	121	15	US-10-468-370-642	Sequence 642, App
20	40	78.4	121	15	US-10-468-370-644	Sequence 644, App
21	40	78.4	121	15	US-10-468-370-646	Sequence 646, App
22	40	78.4	121	15	US-10-468-370-648	Sequence 648, App
23	40	78.4	121	15	US-10-468-370-650	Sequence 650, App
24	40	78.4	121	15	US-10-468-370-652	Sequence 652, App
25	40	78.4	121	15	US-10-468-370-654	Sequence 654, App
26	40	78.4	121	15	US-10-468-370-656	Sequence 656, App
27	40	78.4	121	15	US-10-468-528-1	Sequence 1, Appl
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35	40	78.4	317	16	US-10-437-963-132544	Sequence 132544, A
36	39	76.5	124	9	US-09-864-761-33551	Sequence 33551, A
37	39	76.5	161	9	US-09-821-687-2	Sequence 2, Appl
38	39	76.5	545	9	US-09-978-242-1	Sequence 1, Appl
39	39	76.5	561	9	US-09-821-687-4	Sequence 4, Appl
40	39	76.5	579	9	US-09-925-300-1415	Sequence 1415, Ap
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43	38	74.5	119	15	US-10-389-155-19	Sequence 19, Appl
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57	37	72.5	8	15	US-10-293-418-13092	Sequence 13092, Ap
58	37	72.5	14	9	US-09-252-150-63	Sequence 63, Appl
59	37	72.5	15	9	US-09-252-150-62	Sequence 62, Appl
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62	37	72.5	125	9	US-09-144-886-41	Sequence 41, Appl
63	37	72.5	125	16	US-10-632-706-48	Sequence 48, Appl
64	37	72.5	200	16	US-10-437-963-177565	Sequence 177565, A
65	37	72.5	243	10	US-09-880-748-2102	Sequence 2102, Ap
66	37	72.5	243	15	US-10-293-418-2102	Sequence 2102, Ap
67	37	72.5	673	14	US-10-294-561-3	Sequence 3, Appl
68	37	72.5	1229	16	US-10-437-963-132817	Sequence 132817, A
69	37	72.5	1610	16	US-10-437-963-194199	Sequence 194199, A
70	36	70.6	63	11	US-09-864-408A-416	Sequence 416, App
71	36	70.6	67	15	US-10-264-049-3574	Sequence 3574, Ap
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76	36	70.6	120	9	US-09-229-200A-22	Sequence 22, Appl
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78	36	70.6	120	9	US-09-229-200A-24	Sequence 24, Appl
79	36	70.6	120	9	US-09-229-200A-25	Sequence 25, Appl
80	36	70.6	120	9	US-09-229-200A-26	Sequence 26, Appl
81	36	70.6	120	9	US-09-229-200A-27	Sequence 27, Appl
82	36	70.6	120	9	US-09-229-200A-28	Sequence 28, Appl
83	36	70.6	191	16	US-10-437-963-189083	Sequence 189083, A
84	36	70.6	210	15	US-10-282-122A-52165	Sequence 52165, A
85	36	70.6	301	9	US-09-799-777-64	Sequence 64, Appl
86	36	70.6	425	15	US-10-369-493-1158	Sequence 1158, Ap

87 36 70.6 435 9 US-09-815-242-5283 Sequence 5283, Ap
88 36 70.6 436 9 US-09-815-242-12600 Sequence 12600, A
89 36 70.6 436 9 US-09-815-242-12732 Sequence 12732, A
90 36 70.6 436 15 US-10-282-122A-43793 Sequence 43793, A
91 36 70.6 436 15 US-10-282-122A-70602 Sequence 70602, A
92 36 70.6 436 15 US-10-282-122A-71683 Sequence 71683, A
93 36 70.6 436 17 US-10-857-625-660 Sequence 660, App
94 36 70.6 563 15 US-10-425-114-58931 Sequence 58931, A
95 36 70.6 570 15 US-10-425-114-62721 Sequence 62721, A
96 36 70.6 579 15 US-10-425-114-56520 Sequence 56520, A
97 36 70.6 581 15 US-10-425-114-63215 Sequence 63215, A
98 36 70.6 738 16 US-10-451-467A-238 Sequence 238, App
99 35.5 69.6 123 16 US-10-663-244-15 Sequence 15, Appl
100 35.5 69.6 123 16 US-10-663-244-97 Sequence 97, Appl

ALIGNMENTS

RESULT 1
US-10-018-245A-3
; Sequence 3, Application US/10018245A
; Publication No. US20040115196A1
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, Yoshiaki
; APPLICANT: NAGAHIRA, Kazuhiro
; APPLICANT: NAKANISHI, Yoshihiro
; TITLE OF INVENTION: Novel recombinant antibody, amino acid sequences of its complement
; TITLE OF INVENTION: determining regions and genes encoding the same
; FILE REFERENCE: 46324
; CURRENT APPLICATION NUMBER: US/10/018,245A
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: JP 117394/2000
; PRIOR FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: mouse
; FEATURE:
; OTHER INFORMATION: CDR-H3 of anti-human TNF-alpha antibody
US-10-018-245A-3
Query Match 100.0%; Score 51; DB 16; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YDYDGFY 8
DB 1 YDYDGFY 8
RESULT 2
US-10-472-928-4482
; Sequence 4482, Application US/10472928
; Publication No. US20050020813A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026926W0
; CURRENT APPLICATION NUMBER: US/10/472,928
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: GB-0107656.7
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4979
; SOFTWARE: Seqwin99, version 1.03
; SEQ ID NO 4482
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; FEATURE:

; OTHER INFORMATION: hypothetical protein
; OTHER INFORMATION: Cellular location: Cytoplasm
; OTHER INFORMATION: Similar to strain R6 sequence 15903989 (8.E-63)
US-10-472-928-4482

Query Match 86.3%; Score 44; DB 17; Length 108;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYDGFY 8
DB 99 DYDGFY 105

RESULT 3
US-10-435-299-10
; Sequence 10, Application US/10435299
; Publication No. US20040052783A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Gingrich, Roger
; APPLICANT: Link, Brian
; APPLICANT: Teo, J. Yun
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST CD3
; FILE REFERENCE: 05882-0176-CNUS04
; CURRENT APPLICATION NUMBER: US/10/435,299
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 09/618,380
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 08/397,411
; PRIOR FILING DATE: 1995-03-01
; PRIOR APPLICATION NUMBER: US 07/859,583
; PRIOR FILING DATE: 1992-03-27
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain of Humanized M291 Ab minus signal sequence
US-10-435-299-10
Query Match 84.3%; Score 43; DB 15; Length 120;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YDYDGFY 8
DB 102 YDYDGFY 109
RESULT 4
US-10-435-299-11
; Sequence 11, Application US/10435299
; Publication No. US20040052783A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Gingrich, Roger
; APPLICANT: Link, Brian
; APPLICANT: Teo, J. Yun
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST CD3
; FILE REFERENCE: 05882-0176-CNUS04
; CURRENT APPLICATION NUMBER: US/10/435,299
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 09/618,380
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 08/397,411
; PRIOR FILING DATE: 1995-03-01
; PRIOR APPLICATION NUMBER: US 07/859,583
; PRIOR FILING DATE: 1992-03-27
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:54:17 ; Search time 11.25 Seconds
(without alignments)
68.421 Million cell updates/sec

Title: US-10-018-245A-3
Perfect score: 51
Sequence: 1 YDYDGFY 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	86.3	108	2	C95250
2	44	86.3	108	2	A99715
3	42	82.4	76	2	T28269
4	40.5	79.4	123	2	S60067
5	40	78.4	1322	2	B71440
6	39	76.5	365	2	T68896
7	39	76.5	647	2	F70057
8	38	74.5	106	1	NNASTP
9	38	74.5	117	2	S17586
10	38	74.5	123	2	B30560
11	38	74.5	282	2	T35294
12	38	74.5	493	2	S78384
13	37	72.5	195	2	D84364
14	37	72.5	673	2	A49878
15	36	70.6	210	2	G97235
16	36	70.6	231	2	E90002
17	36	70.6	257	2	S50288
18	36	70.6	301	2	JM0079
19	36	70.6	321	2	A69088
20	36	70.6	391	2	T54530
21	36	70.6	425	2	F69193
22	36	70.6	436	2	C89926
23	36	70.6	540	2	T00463
24	36	70.6	559	2	A42807
25	36	70.6	560	2	T32288
26	36	70.6	607	2	S24754
27	36	70.6	738	2	S37876
28	36	70.6	752	2	H86770
29	36	70.6	1198	2	T49726

30	35	68.6	91	2	I58989	MHC H2-K transplan
31	35	68.6	91	2	I59068	MHC class I H2-K-b
32	35	68.6	109	2	S26325	Ig heavy chain V r
33	35	68.6	131	2	A27472	Ig heavy chain pre
34	35	68.6	163	2	C81283	flavodoxin Cj182c
35	35	68.6	180	2	S37891	hypothetical prote
36	35	68.6	201	2	C40040	alternative splici
37	35	68.6	201	2	S26404	H-2 class I histoc
38	35	68.6	206	2	JL0059	conserved hypothet
39	35	68.6	216	2	A64962	hypothetical prote
40	35	68.6	216	2	F85815	hypothetical prote
41	35	68.6	216	2	G90967	hypothetical prote
42	35	68.6	235	2	T47379	alternative splici
43	35	68.6	248	2	A40040	protein containing
44	35	68.6	255	2	G97227	alternative splici
45	35	68.6	292	2	B40040	conserved hypothet
46	35	68.6	319	2	H69043	hypothetical prote
47	35	68.6	323	2	T32874	hypothetical prote
48	35	68.6	328	1	E54392	npp protein - Ent
49	35	68.6	353	1	S56750	single stranded D
50	35	68.6	360	2	A27638	MHC class I histoc
51	35	68.6	361	1	HLRB	MHC class I histoc
52	35	68.6	361	2	I46858	MHC class I RLA pr
53	35	68.6	362	2	A45849	MHC class I histoc
54	35	68.6	362	2	A45876	MHC class I histoc
55	35	68.6	365	2	I57814	MHC class I-alpha
56	35	68.6	369	1	HLMSKB	MHC class I histoc
57	35	68.6	369	1	HLMSKB	MHC class I histoc
58	35	68.6	422	2	G72227	hypothetical prote
59	35	68.6	474	1	G2MS11	Ig gamma-2b chain
60	35	68.6	876	2	B90547	lipoprotein (impor
61	35	68.6	1385	2	H88569	protein K03H1.5 [i
62	35	68.6	1409	2	S41028	hypothetical prote
63	34	66.7	118	2	AB2104	hypothetical prote
64	34	66.7	137	2	I80172	class I histoccompa
65	34	66.7	137	2	I80175	class I histoccompa
66	34	66.7	137	2	I80176	class I histoccompa
67	34	66.7	137	2	I80174	class I histoccompa
68	34	66.7	181	2	I59188	MHC cell surface g
69	34	66.7	203	2	E81449	hypothetical prote
70	34	66.7	206	2	I37528	HLA-Cw1 - human (I
71	34	66.7	210	2	S73509	MHC class I HLA-J
72	34	66.7	218	2	I72808	class I-related se
73	34	66.7	241	1	HLMSPR	MHC H2-K1-k - mus
74	34	66.7	243	2	I54459	MHC HLA-A cell sur
75	34	66.7	246	2	I54412	MHC class I histoc
76	34	66.7	273	1	HLH069	MHC class I histoc
77	34	66.7	276	2	I38509	MHC class I histoc
78	34	66.7	276	2	T52316	chlorophyll a/b-bi
79	34	66.7	305	2	S07115	class I histoccompa
80	34	66.7	308	2	I36956	MHC class I histoc
81	34	66.7	322	2	A21125	MHC class I histoc
82	34	66.7	325	2	S20045	MHC class I histoc
83	34	66.7	329	2	A40730	MHC class I histoc
84	34	66.7	338	2	A39953	MHC HLA-B27-HS - h
85	34	66.7	338	2	I56116	MHC class I histoc
86	34	66.7	339	2	I56071	heterogeneous nucl
87	34	66.7	345	1	B41732	MHC HLA B71 - huma
88	34	66.7	350	2	I54308	MHC class I lympho
89	34	66.7	350	2	I68747	hypothetical prote
90	34	66.7	353	2	F64175	class I histoccompa
91	34	66.7	354	2	S24438	class I histoccompa
92	34	66.7	354	2	S24436	class I histoccompa
93	34	66.7	355	2	B40730	class I histoccompa
94	34	66.7	355	2	I80171	class I histoccompa
95	34	66.7	355	2	I80169	class I histoccompa
96	34	66.7	357	2	I11136	class I histoccompa
97	34	66.7	357	2	S11133	class I histoccompa
98	34	66.7	357	2	S11140	class I histoccompa
99	34	66.7	357	2	AD1062	protein kinase (im
100	34	66.7	358	2	S03538	class I histoccompa

ALIGNMENTS

RESULT 1

hypothetical protein SP2139 [imported] - Streptococcus pneumoniae (strain TIGR4)

C/Species: Streptococcus pneumoniae
C/Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C/Accession: G95250
R/Retelink: H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidon, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A/Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A./Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A/Reference number: A95000; MUID:21357209; PMID:11463916
A/Accession: G95250
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-108 <KUR>
A/Cross-references: UNIPROT:Q97NB3; GB:AE005672; PIDN:AAK76196.1; PID:G14973651; GSPDB:C
A/Experimental source: strain TIGR4
C/Genetics:
A/Gene: SP2139

Query Match 86.3%; Score 44; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYDGFY 8
|||||
Db 99 DYDGFY 105

RESULT 2

A99715
hypothetical protein spr1948 [imported] - Streptococcus pneumoniae (strain R6)

C/Species: Streptococcus pneumoniae
C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C/Accession: A99715
R/Hoskins, J.A.; Albhorn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; Ee, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; My, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A/Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A/Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A/Reference number: A97872; MUID:21429245; PMID:11544234
A/Accession: A99715
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-108 <KUR>
A/Cross-references: UNIPROT:Q8CY66; GB:AE007317; PIDN:AAU00750.1; PID:G15459647; GSPDB:C
C/Genetics:
A/Gene: spr1948

Query Match 86.3%; Score 44; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYDGFY 8
|||||
Db 99 DYDGFY 105

RESULT 3

T28269
ORF MSV108 hypothetical protein - Melanoplus sanguinipes entomopoxvirus

C/Species: Melanoplus sanguinipes entomopoxvirus
C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C/Accession: T28269
R/Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A/Title: The genome of Melanoplus sanguinipes entomopoxvirus.

A/Reference number: Z20484; MUID:99102612; PMID:9847359
A/Accession: T28269
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-76 <AFO>
A/Cross-references: UNIPROT:Q9YVY4; EMBL:AF063866; NID:G4049647; PIDN:AAQ7654.1; PID:G4
C/Genetics:
A/Note: MSV108

Query Match 82.4%; Score 42; DB 2; Length 76;
Best Local Similarity 87.5%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YDVGFDY 8
|||||
Db 38 YDVGFDY 45

RESULT 4

S60067
Ig heavy chain V region (monoclonal antibody C3, gamma 2a) [validated] - mouse (fragment)

C/Species: Mus musculus (house mouse)
C/Date: 23-Feb-1996 #sequence_revision 10-Oct-1997 #text_change 23-Mar-2001
C/Accession: S60067
R/Wien, M.W.; Filman, D.J.; Stura, E.A.; Guillot, S.; Delpeyroux, F.; Crainic, R.; Hogle, Nat. Struct. Biol. 2, 232-243, 1995
A/Title: Structure of the complex between the Fab fragment of a neutralizing antibody for A/Reference number: S60066; MUID:95292109; PMID:7539711
A/Accession: S60067
A/Molecule type: mRNA
A/Residues: 1-123 <WIB>
A/Cross-references: EMBL:X04698; NID:G773225
R/Wien, M.W.; Hogle, J.M.
submitted to the Brookhaven Protein Data Bank, January 1995
A/Contents: annotation: X-ray crystallography, 3.0 angstroms, residues 1-123
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin; pyroglytamic acid
F/15-98/Domain: immunoglobulin homology <IMM>
F/1/Modified site: pyroglutamate carboxylic acid (Gln) #status predicted
F/22-96/Disulfide bonds: #status experimental

Query Match 79.4%; Score 40.5; DB 2; Length 123;
Best Local Similarity 88.9%; Pred. No. 5.8;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 YDVGFDY 8
|||||
Db 101 YDVGFDY 109

RESULT 5

B71440
hypothetical protein d14605c - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)
A/Variety: Columbia
C/Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
C/Accession: B71440
R/Beran, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenecker, T.; Pohl, T.M.; Terry, N.; Giete avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B. Nature 391, 485-488, 1998
A/Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech, erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Anst C.; Chaiwatizis, N.
A/Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal

A/Reference number: A71400; MUID:98121113; PMID:9461215
A/Accession: B71440
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-1322 <BEV>
A/Cross-references: UNIPROT:O2J559; GB:Z97342; NID:G2245031; PID:G2245072
C/Genetics:

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:54:17 ; Search time 52.75 Seconds
(without alignments)
77.661 Million cell updates/sec

Title: US-10-018-245A-3
Perfect score: 51
Sequence: 1 YDYDGFY 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : UniProt 03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	86.3	91	2	005165 streptococc
2	44	86.3	108	2	097NB3 streptococc
3	44	86.3	108	2	08CY66 streptococc
4	44	86.3	348	2	064Q75 bacteroides
5	44	86.3	560	2	043319 attemisia a
6	44	86.3	561	2	06DFC0 xenopus lae
7	43	84.3	363	2	09HC87 homo sapien
8	43	84.3	542	2	09QZT6 mus musculu
9	43	84.3	728	2	09RIY8 mus musculu
10	43	84.3	736	2	096SK8 homo sapien
11	43	84.3	736	2	096SL5 homo sapien
12	43	84.3	736	2	09HC86 homo sapien
13	43	84.3	738	2	08BSV2 mus musculu
14	43	84.3	739	2	08CFJ3 mus musculu
15	43	84.3	742	2	09CMK5 mus musculu
16	43	84.3	747	2	09QZT7 mus musculu
17	43	84.3	765	2	06NT19 xenopus lae
18	43	84.3	804	2	096SN3 homo sapien
19	42	82.4	76	2	09YVY4 melanoplus
20	42	82.4	772	2	08RGC0 fusobacteri
21	41	80.4	758	2	06F7M5 actinobact
22	41	80.4	1658	2	091BW3 indian citr
23	40	78.4	308	2	073S89 mycobacteri
24	40	78.4	574	2	017411 aedes aegypt
25	40	78.4	1126	2	073ME8 treponema d
26	40	78.4	1322	2	023559 arabidopsis
27	40	78.4	3320	2	073MR0 treponema d
28	39	76.5	365	2	06Z585 peromyseus
29	39	76.5	367	2	08A1B3 bacteroides
30	39	76.5	533	1	ROQ_RAT
31	39	76.5	561	2	068ED6 mus musculu

32	39	76.5	623	1	ROQ_HUMAN	060506 homo sapien
33	39	76.5	623	1	ROQ_MOUSE	07cmx9 mus musculu
34	39	76.5	624	2	06NS22 xenopus lae	06ns22 xenopus lae
35	39	76.5	630	2	06NUZ3	06nu23 brachydanio
36	39	76.5	647	2	070997	070997 bacillus su
37	39	76.5	725	2	06UH08	06uhus gallus gall
38	39	76.5	772	2	07P394	07p394 fusobacteri
39	38	74.5	105	1	RNMS_ASPPSA	P06653 aspergillus
40	38	74.5	282	2	06WDT7	06wdt7 euryymna sc
41	38	74.5	282	2	09S208	09s2q8 streptomyce
42	38	74.5	283	2	06WDS	06wdns euryymna sc
43	38	74.5	283	2	06WDN8	06wdns euryymna sc
44	38	74.5	284	2	06WDN2	06wdn2 euryymna sc
45	38	74.5	284	2	06WDN3	06wdn3 euryymna sc
46	38	74.5	284	2	06WDN4	06wdn4 euryymna sc
47	38	74.5	327	1	MTX1_DROME	09vhs6 drosophila
48	38	74.5	340	2	08A8X9	08a8x9 bacteroides
49	38	74.5	360	2	07P891	07p891 fusobacteri
50	38	74.5	375	2	087448	087448 chimpanzee
51	38	74.5	385	2	0650Y1	0650y1 oryza sativ
52	38	74.5	435	2	06TMJ7	06tmj7 dictyosteli
53	38	74.5	435	2	0861R2	0861r2 dictyosteli
54	38	74.5	493	1	ACCD_EPIVI	P30064 epilegus vi
55	38	74.5	695	2	052863	052863 sodalis glo
56	37	72.5	158	2	06CWR0	06cwr0 kluyveromyc
57	37	72.5	184	2	081ZD4	081ztd bacillus an
58	37	72.5	189	2	061480	061480 bacillus an
59	37	72.5	195	1	VATE_HAANI	09hneo halobacteri
60	37	72.5	260	1	TRUA_SPIKU	P60353 epiloplasma
61	37	72.5	291	2	06NU14	06nu14 xenopus lae
62	37	72.5	295	2	0645K2	0645k2 xenopus lae
63	37	72.5	296	2	07SXN2	07sxn2 brachydanio
64	37	72.5	297	2	0640A2	0640a2 xenopus tro
65	37	72.5	305	2	08PW15	08pw15 methanosaic
66	37	72.5	344	2	061893	061893 mus musculu
67	37	72.5	350	2	064WP9	064wp9 bacteroides
68	37	72.5	375	2	08A8W9	08a8w9 bacteroides
69	37	72.5	673	2	027082	027082 tachypleus
70	37	72.5	742	2	06CIN7	06cin7 kluyveromyc
71	37	72.5	931	2	06CB39	06cb39 yarrowia li
72	37	72.5	1025	2	09V636	09v636 drosophila
73	37	72.5	1040	2	09LNG0	09lng0 arabidopsis
74	37	72.5	2514	2	07RD79	07rd79 plasmodium
75	37	72.5	4099	2	09C7Z6	09c7z6 arabidopsis
76	36	70.6	79	2	06X9Z3	06x9z3 equus caball
77	36	70.6	105	2	09AFB6	09afb6 anaerococcu
78	36	70.6	110	2	09AFB7	09afb7 anaerococcu
79	36	70.6	110	2	09AFB9	09afb9 anaerococcu
80	36	70.6	111	2	09AFB4	09afb4 anaerococcu
81	36	70.6	210	2	07YNZ6	07ynz6 sus scrofa
82	36	70.6	210	2	097PK9	097fk9 clostridium
83	36	70.6	231	2	08NVH0	08nvho staphylococ
84	36	70.6	231	2	09SGS2	09sgs2 staphylococ
85	36	70.6	231	2	07A4P2	07a4f2 staphylococ
86	36	70.6	231	2	06G7L4	06g7l4 staphylococ
87	36	70.6	231	2	06GEX9	06gex9 staphylococ
88	36	70.6	254	2	09XYT0	09xyt0 rhizopertha
89	36	70.6	256	2	09TPK9	09tpk9 quiplex monodelphis
90	36	70.6	257	1	YBE3_YEAST	P81195 saccharomyc
91	36	70.6	271	2	07XZK74	07kz74 homo sapien
92	36	70.6	293	2	07XZK83	07kz83 homo sapien
93	36	70.6	298	2	06SPR2	06spr2 homo sapien
94	36	70.6	301	2	07KZ75	07kz75 homo sapien
95	36	70.6	301	2	09Z130	09z130 mus musculu
96	36	70.6	308	2	088AB4	088ab4 pseudomonas
97	36	70.6	321	2	027690	027690 methanobact
98	36	70.6	339	2	086F19	086f19 schistosoma
99	36	70.6	349	2	06CL42	06cl42 kluyveromyc
100	36	70.6	356	1	AROB_THETN	06rb14 thermocanaer

ALIGNMENTS

RESULT 1

005165 ID 005165 PRELIMINARY; PRT; 91 AA.
AC 005165;
DT 01-JUN-1997 (TREMblrel. 04, Last Created)
DT 01-JUN-1997 (TREMblrel. 04, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Hypothetical protein.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_Taxid=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6;
RX MEDLINE=98340517; PubMed=9675866;
RA Sanchez-Beato A., Lopez R., Garcia J.;
RT "Molecular characterization of PcpA: a novel choline-binding protein
of Streptococcus pneumoniae."
RL FEMS Microbiol. Lett. 164:207-214 (1998).
DR EMBL; Z82001; CAB04757.1; -.
KM Hypothetical protein.
SQ SEQUENCE 91 AA; 11056 MW; 7CA9A5C88F33A585 CRC64;

Query Match 86.3%; Score 44; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DYDGFY 8
Db 82 DYDGFY 88

RESULT 2

097NB3 ID 097NB3 PRELIMINARY; PRT; 108 AA.
AC 097NB3;
DT 01-OCT-2001 (TREMblrel. 18, Created)
DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Hypothetical protein SP2139.
GN OrderedLocustNames=SP2139.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_Taxid=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC BAA-334 / TIGR4;
RX MEDLINE=21357209; PubMed=11463916; DOI=10.1126/science.1061217;
RA Tetteijn H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S.N., Heidelberg J.F., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin L.A., Ghann M.L., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Kadane D.,
RA Holtzapfe E.K., Knout H.M., Wolf A.M., Uletterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiolini S.V., Dickinson T.,
RA Hickey E.K., Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
pneumoniae."
RL Science 293:498-506 (2001).
DR EMBL; AE007502; AAK76196.1; -.
DR PIR; C95250; C95250.
DR TIGR; SP2139; -.
KM Complete proteome; Hypothetical protein
SQ SEQUENCE 108 AA; 13150 MW; 218F51E4BDAF20A CRC64;

Query Match 86.3%; Score 44; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DYDGFY 8

Db 99 DYDGFY 105

RESULT 3

08CY66 ID 08CY66 PRELIMINARY; PRT; 108 AA.
AC 08CY66;
DT 01-MAR-2003 (TREMblrel. 23, Created)
DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Hypothetical protein spr1948.
GN OrderedLocustNames=spr1948;
OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_Taxid=171101;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21429245; PubMed=11544234;
RX DOI=10.1128/JB.183.19.5709-5717.2001;
RA Hoskins J., Alborn W.E., Jr., Arnold J., Blaszcak L.C., Burgett S.,
RA Dehoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
RA Gilmore R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
RA Leblanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
RA McAhren S.M., McHenry M., McKeaster K., Mundy C.W., Niclas T.I.,
RA Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rokey P.,
RA Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
RA Zook C.A., Baltz R.H., Jaskunas S.R., Rostek P.R., Jr., Skatrud P.L.,
RA Glass J.I.;
RT "Genome of the bacterium Streptococcus pneumoniae strain R6."
RL J. Bacteriol. 183:5709-5717 (2001).
DR EMBL; AE008559; AAL00750.1; -.
DR PIR; A99715; A99715.
KM Complete proteome.
SQ SEQUENCE 108 AA; 13107 MW; 362F4644B8C30DEC CRC64;

Query Match 86.3%; Score 44; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DYDGFY 8
Db 99 DYDGFY 105

RESULT 4

064075 ID 064075 PRELIMINARY; PRT; 348 AA.
AC 064075;
DT 25-OCT-2004 (TREMblrel. 28, Created)
DT 25-OCT-2004 (TREMblrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMblrel. 28, Last annotation update)
DE Putative endo-beta-N-acetylglucosaminidase.
GN ORFNames=BF3613;
OS Bacteroides fragilis.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_Taxid=817;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YCH46;
RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kuhara S., Hattori M., Hayashi T., Ohnishi Y.;
RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
inversions regulating cell surface adaptation."
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0 (2004).
DR EMBL; AP006841; BAD50356.1; -.
SQ SEQUENCE 348 AA; 39951 MW; 5ADA0761BF73EEF3 CRC64;

Query Match 86.3%; Score 44; DB 2; Length 348;
Best Local Similarity 87.5%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:54:17 ; Search time 91.125 Seconds
(without alignments)
50.931 Million cell updates/sec

Title: US-10-018-245A-4
Perfect score: 58
Sequence: 1 TASSSVSFYSLH 12

Scoring table: BLASTSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 100 summaries

Database :

- 1: A_Geneseq_16Dec04:*
- 2: geneseqp1980s:*
- 3: geneseqp1990s:*
- 4: geneseqp2000s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	12	5	AAG80314
2	58	100.0	108	5	AAG80318
3	50	86.2	12	3	AAH10004
4	50	86.2	12	8	ADJ25666
5	50	86.2	12	8	ADJ25666
6	50	86.2	108	8	AAH10021
7	50	86.2	108	8	ADJ25650
8	50	86.2	129	8	ADJ25650
9	50	86.2	129	8	ADJ25650
10	47	81.0	109	8	ADQ31871
11	47	81.0	109	8	ADQ31871
12	47	81.0	109	8	ADQ31867
13	47	81.0	109	8	ADQ31867
14	47	81.0	109	8	ADQ31870
15	47	81.0	130	8	ADQ31877
16	47	81.0	130	8	ADQ31866
17	47	81.0	130	8	ADQ31881
18	47	81.0	215	8	ADQ31885
19	47	81.0	215	8	ADQ31891
20	46	79.3	12	5	AAU70355
21	46	79.3	108	8	AAV53591
22	46	79.3	110	2	AAW46482
23	46	79.3	130	2	AAW73291
24	46	79.3	215	8	ADN97547
25	46	79.3	483	8	ADN97549

26	46	79.3	826	2	AAV30101
27	45	77.6	12	4	AAH81967
28	45	77.6	57	6	ABU56885
29	45	77.6	108	3	AAV59306
30	45	77.6	109	4	AAH81974
31	45	77.6	109	4	AAH81971
32	45	77.6	110	2	AAH21307
33	45	77.6	110	2	AAH21306
34	45	77.6	110	2	AAH21287
35	45	77.6	131	4	AAH81976
36	45	77.6	195	2	AAH06477
37	45	77.6	214	5	AAH76125
38	45	77.6	215	2	AAH43674
39	45	77.6	215	2	AAH99644
40	45	77.6	215	2	AAH97377
41	45	77.6	225	2	AAH05710
42	45	77.6	225	2	AAH06478
43	45	77.6	225	2	AAH43675
44	45	77.6	225	2	AAH99645
45	45	77.6	236	2	AAH06479
46	45	77.6	236	2	AAH43676
47	45	77.6	236	2	AAH99646
48	45	77.6	236	2	AAH02188
49	45	77.6	239	2	AAH43679
50	45	77.6	239	2	AAH99649
51	45	77.6	239	2	AAH02191
52	45	77.6	241	2	AAH06482
53	45	77.6	242	2	AAH06483
54	45	77.6	242	2	AAH43680
55	45	77.6	242	2	AAH99650
56	45	77.6	242	2	AAH02192
57	45	77.6	246	2	AAH06480
58	45	77.6	246	2	AAH43677
59	45	77.6	246	2	AAH99647
60	45	77.6	246	2	AAH02189
61	45	77.6	250	2	AAH43678
62	45	77.6	250	2	AAH99648
63	45	77.6	250	2	AAH02190
64	45	77.6	951	3	AAV44993
65	45	77.6	44	7	ADH62642
66	45	77.6	45	7	ADH62641
67	45	77.6	45	7	ADH62640
68	45	77.6	57	6	ABU56841
69	45	77.6	57	6	ABU56842
70	45	77.6	60	4	AAU49473
71	45	77.6	60	4	AAU49473
72	45	77.6	103	2	AAV05362
73	45	77.6	109	2	AAH79864
74	45	77.6	109	2	AAH79864
75	45	77.6	109	2	AAH79864
76	45	77.6	109	8	ADR38687
77	45	77.6	109	8	ADR38692
78	45	77.6	110	2	AAH21288
79	45	77.6	110	2	AAH21297
80	45	77.6	110	2	AAH21299
81	45	77.6	110	2	AAH21295
82	45	77.6	110	2	AAH21289
83	45	77.6	110	2	AAH21300
84	45	77.6	239	2	AAV17963
85	45	77.6	240	8	ADR59121
86	45	77.6	245	2	AAW25783
87	45	77.6	255	5	AAU72866
88	45	77.6	255	5	AAU72866
89	45	77.6	297	2	AAV05363
90	45	77.6	315	4	AAH70843
91	45	77.6	503	5	AAU72874
92	45	77.6	708	8	ADJ49669
93	45	77.6	742	2	AAW53881
94	45	77.6	742	2	AAW53882
95	45	77.6	12	8	ADH25804
96	45	77.6	12	8	ADH59661
97	45	77.6	108	8	ADH59682
98	45	77.6	108	8	ADH59675

AAV30101	An acetyl
AAH81967	Ganglios
ABU56885	BONT/A Hc
AAV59306	DC8 light
AAH81974	Ganglios
AAH81971	Ganglios
AAH21307	Murine VL
AAH21306	Murine VL
AAH21287	Murine VL
AAH81976	Ganglios
AAH06477	Light cha
AAH76125	Recombina
AAH43674	Mouse ant
AAH99644	Anti-DGH
AAH97377	Murine an
AAH05710	TRY40. 9/
AAH06478	TRY40. 3/
AAH43675	Single ch
AAH99645	Single ch
AAH06479	TRY61. 3/
AAH43676	Single ch
AAH99646	Single ch
AAH02188	TRY61 sin
AAH43679	Single ch
AAH99649	Single ch
AAH02191	18-2-3/TR
AAH06482	18-2-3/-T
AAH06483	18-2-3/-T
AAH43680	Single ch
AAH99650	Single ch
AAH02192	18-2-3/TR
AAH06480	TRY59. 3/
AAH43677	Single ch
AAH99647	Single ch
AAH02189	TRY59 sin
AAH43678	Single ch
AAH99648	Single ch
AAH02190	TRY104b s
AAV44993	DC8CFV-e
ADH62642	Mouse ant
ADH62641	Mouse ant
ADH62640	Mouse ant
ABU56841	BONT/A Hc
ABU56842	BONT/A Hc
AAU49473	Propionib
AAH45892	Propionib
AAV05362	HBV speci
AAH79864	Anti-EGFR
AAH79864	Human IGE
AAW25783	Thyroid h
ADR38687	Mouse lig
ADR38692	Mouse lig
AAH21288	Murine VL
AAH21297	Murine VL
AAH21299	Murine VL
AAH21295	Murine VL
AAH21289	Murine VL
AAH21300	Murine VL
AAV17963	Mouse scf
ADR59121	Anti-X88/
AAW25783	Anti-T3 a
AAU72866	PS-3 sing
AAV05363	HBV speci
AAH70843	SNV-ent
AAU72874	3B10XP5-2
ADJ49669	Oil-assoc
AAW53881	Firefly I
AAW53882	Antibody-
ADH25804	Anti-alph
ADH59661	Light cha
ADH59682	Light cha
ADH59675	Anti-alph

99 40 69.0 108 8 ADH59680
100 40 69.0 108 8 ADH59704

ADH59680 Chimeric
ADH59704 PAM4 VK P

ALIGNMENTS

RESULT 1
AAG80314
ID AAG80314 standard; peptide; 12 AA.
XX

AC AAG80314;

XX 18-FEB-2002 (first entry)

DE Anti-human TNF-alpha CDR-L1 peptide.

XX TNF-alpha; tumour necrosis factor-alpha; antibody; anti-human; CDR;
KW heavy chain; light chain; complementarity determining region; vasotropic;
KW antiarthritic; neuroprotective; protozoacide; toxic shock syndrome;
KW rheumatoid arthritis; malaria; multiple sclerosis.

XX Homo sapiens.

XX WO200179298-A1.

XX 25-OCT-2001.

XX 18-APR-2001; 2001WO-JP003308.

XX 19-APR-2000; 2000JP-00117394.

XX (SUNR) SUNTORY LTD.

XX Fukuda Y, Nagahira K, Nakanishi T;

XX WPI; 2002-066345/09.

XX Novel heavy and light-chain polypeptides of chimeric and humanized
PT antibodies against human tumor necrosis factor alpha for low-
PT immunogenicity treatment of TNF-related diseases such as toxic shock
PT syndrome.

XX Claim 3a; Page 26; 36pp; Japanese.

XX This invention describes novel heavy chain and light chain polypeptides
or their fragments of a recombinant antibody to human TNF-alpha which
contain complementarity determining region (CDR) sequences. The products
of the invention have vasotropic, antiarthritic, neuroprotective and
protozoacide activity. The antibodies act by neutralising TNF-alpha in
vivo. The antibodies are used for producing chimeric and humanised
antibodies that may be used for the treatment and prevention of TNF-alpha
associated diseases such as toxic shock syndrome, rheumatoid arthritis,
malaria and multiple sclerosis. The antibodies have low immunogenicity in
humans. This sequence represents the anti-human tumour necrosis factor-
alpha (TNF-alpha) light chain CDR1 designated CDR-L1

XX Sequence 12 AA;

Query Match 100.0%; Score 58; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TASSVSFSYLH 12
|||
Db 1 TASSVSFSYLH 12

RESULT 2
AAG80318
ID AAG80318 standard; protein; 108 AA.
XX
AC AAG80318;

XX 18-FEB-2002 (first entry)

DE Anti-human TNF-alpha L chain CDR region encoding DNA.

XX TNF-alpha; tumour necrosis factor-alpha; antibody; anti-human; CDR;
KW heavy chain; light chain; complementarity determining region; vasotropic;
KW antiarthritic; neuroprotective; protozoacide; toxic shock syndrome;
KW rheumatoid arthritis; malaria; multiple sclerosis.

XX Homo sapiens.

XX WO200179298-A1.

XX 25-OCT-2001.

XX 18-APR-2001; 2001WO-JP003308.

XX 19-APR-2000; 2000JP-00117394.

XX (SUNR) SUNTORY LTD.

XX Fukuda Y, Nagahira K, Nakanishi T;

XX WPI; 2002-066345/09.

XX N-PSDB; AAI69376.

XX Novel heavy and light-chain polypeptides of chimeric and humanized
PT antibodies against human tumor necrosis factor alpha for low-
PT immunogenicity treatment of TNF-related diseases such as toxic shock
PT syndrome.

XX Disclosure; Page 28-29; 36pp; Japanese.

XX This invention describes novel heavy chain and light chain polypeptides
or their fragments of a recombinant antibody to human TNF-alpha which
contain complementarity determining region (CDR) sequences. The products
of the invention have vasotropic, antiarthritic, neuroprotective and
protozoacide activity. The antibodies act by neutralising TNF-alpha in
vivo. The antibodies are used for producing chimeric and humanised
antibodies that may be used for the treatment and prevention of TNF-alpha
associated diseases such as toxic shock syndrome, rheumatoid arthritis,
malaria and multiple sclerosis. The antibodies have low immunogenicity in
humans. This sequence represents the anti-human tumour necrosis factor-
alpha (TNF-alpha) light chain CDR fragment described in the invention

XX Sequence 108 AA;

Query Match 100.0%; Score 58; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TASSVSFSYLH 12
|||
Db 24 TASSVSFSYLH 35

RESULT 3
AAB10004
ID AAB10004 standard; protein; 12 AA.

AC AAB10004;

DT 01-NOV-2000 (first entry)

DE H. pylori 26 kDa protein-binding antibody light chain CDR1 peptide.

XX Acid-resistant microorganism; detection; faecal; intestine; infection;
KW monoclonal antibody; light chain; complementarity determining region;
KW CDR.

XX Unidentified.

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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:57:11 ; Search time 24.1875 Seconds
(without alignments)
37.035 Million cell updates/sec

Title: US-10-018-245A-4
Perfect score: 58
Sequence: 1 TASSSVSFSYLH 12

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :
1: Issued Patents AA: *
2: /cgn2_6/ptodata/1/iaa/5A_COMB.pep: *
3: /cgn2_6/ptodata/1/iaa/5B_COMB.pep: *
4: /cgn2_6/ptodata/1/iaa/6A_COMB.pep: *
5: /cgn2_6/ptodata/1/iaa/6B_COMB.pep: *
6: /cgn2_6/ptodata/1/iaa/6CTUS_COMB.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	86.2	244	1	US-08-230-843-2
2	50	86.2	244	2	US-08-636-936-2
3	46	79.3	12	4	US-09-563-222C-35
4	46	79.3	130	2	US-08-659-567-2
5	46	79.3	231	1	US-08-681-432-1
6	45	77.6	110	4	US-09-726-219A-237
7	45	77.6	214	4	US-09-653-755A-5
8	45	77.6	215	6	5455030-3
9	45	77.6	215	6	5455030-3
10	45	77.6	225	6	5455030-5
11	45	77.6	225	6	5455030-5
12	45	77.6	236	6	5455030-7
13	45	77.6	236	6	5455030-7
14	45	77.6	239	6	5455030-13
15	45	77.6	239	6	5455030-13
16	45	77.6	242	6	5455030-15
17	45	77.6	242	6	5455030-15
18	45	77.6	247	6	5455030-9
19	45	77.6	247	6	5455030-9
20	45	77.6	248	6	5455030-11
21	45	77.6	248	6	5455030-11
22	43	74.1	110	4	US-09-726-219A-256
23	43	74.1	110	4	US-09-726-219A-257
24	42	72.4	103	4	US-09-486-814A-6
25	42	72.4	109	2	US-08-553-457A-14
26	42	72.4	109	4	US-09-232-290-7
27	42	72.4	110	4	US-09-726-219A-238

28	42	72.4	110	4	US-09-726-219A-239	Sequence 239, App
29	42	72.4	110	4	US-09-726-219A-245	Sequence 245, App
30	42	72.4	110	4	US-09-726-219A-246	Sequence 246, App
31	42	72.4	110	4	US-09-726-219A-247	Sequence 247, App
32	42	72.4	110	4	US-09-726-219A-249	Sequence 249, App
33	42	72.4	110	4	US-09-726-219A-250	Sequence 250, App
34	42	72.4	110	4	US-09-726-219A-258	Sequence 258, App
35	42	72.4	110	4	US-09-486-814A-2	Sequence 2, Appli
36	39	67.2	108	3	US-08-483-749A-8	Sequence 8, Appli
37	38	65.5	109	2	US-08-002-324-4	Sequence 4, Appli
38	38	65.5	109	5	PCT-US94-00261-4	Sequence 4, Appli
39	37	63.8	111	1	US-08-432-594-2	Sequence 2, Appli
40	37	63.8	111	1	US-08-432-594-4	Sequence 4, Appli
41	37	63.8	111	1	US-08-432-594-14	Sequence 14, Appli
42	37	63.8	106	1	US-07-634-278-1	Sequence 1, Appli
43	37	63.8	106	1	US-07-634-278-7	Sequence 7, Appli
44	37	63.8	106	1	US-07-634-278-8	Sequence 8, Appli
45	37	63.8	106	1	US-07-634-278-16	Sequence 16, Appli
46	37	63.8	106	1	US-08-477-728-1	Sequence 1, Appli
47	37	63.8	106	1	US-08-477-728-7	Sequence 7, Appli
48	37	63.8	106	1	US-08-477-728-8	Sequence 8, Appli
49	37	63.8	106	1	US-08-477-728-16	Sequence 16, Appli
50	37	63.8	106	1	US-08-474-040-1	Sequence 1, Appli
51	37	63.8	106	1	US-08-474-040-7	Sequence 7, Appli
52	37	63.8	106	1	US-08-474-040-8	Sequence 8, Appli
53	37	63.8	106	1	US-08-474-040-16	Sequence 16, Appli
54	37	63.8	106	1	US-08-487-200-1	Sequence 1, Appli
55	37	63.8	106	1	US-08-487-200-7	Sequence 7, Appli
56	37	63.8	106	1	US-08-487-200-8	Sequence 8, Appli
57	37	63.8	106	1	US-08-487-200-16	Sequence 16, Appli
58	37	63.8	106	1	US-08-488-113B-163	Sequence 163, App
59	37	63.8	106	1	US-08-488-113B-165	Sequence 165, App
60	37	63.8	106	1	US-08-477-484B-163	Sequence 163, App
61	37	63.8	106	1	US-08-477-484B-165	Sequence 165, App
62	37	63.8	106	1	US-08-107-669D-49	Sequence 49, App
63	37	63.8	106	1	US-08-107-669D-51	Sequence 51, App
64	37	63.8	106	1	US-08-107-669D-83	Sequence 83, App
65	37	63.8	106	1	US-08-472-788A-84	Sequence 84, App
66	37	63.8	106	2	US-08-472-788A-89	Sequence 49, App
67	37	63.8	106	2	US-08-477-531B-49	Sequence 49, App
68	37	63.8	106	2	US-08-477-531B-51	Sequence 51, App
69	37	63.8	106	2	US-08-646-360-163	Sequence 163, App
70	37	63.8	106	2	US-08-646-360-165	Sequence 165, App
71	37	63.8	106	2	US-08-082-842A-83	Sequence 83, Appli
72	37	63.8	106	2	US-08-082-842A-84	Sequence 84, Appli
73	37	63.8	106	3	US-08-934-841-2	Sequence 2, Appli
74	37	63.8	106	3	US-08-393-409-2	Sequence 2, Appli
75	37	63.8	106	3	US-08-839-765-163	Sequence 163, App
76	37	63.8	106	3	US-08-839-765-165	Sequence 165, App
77	37	63.8	106	3	US-09-136-389-163	Sequence 163, App
78	37	63.8	106	3	US-09-136-389-165	Sequence 165, App
79	37	63.8	106	3	US-08-484-537-1	Sequence 1, Appli
80	37	63.8	106	3	US-08-484-537-7	Sequence 7, Appli
81	37	63.8	106	3	US-08-484-537-16	Sequence 16, Appli
82	37	63.8	106	3	US-08-484-537-163	Sequence 163, App
83	37	63.8	106	3	US-09-610-838-165	Sequence 165, App
84	37	63.8	106	3	US-09-610-838-163	Sequence 163, App
85	37	63.8	106	4	US-09-711-485-163	Sequence 163, App
86	37	63.8	106	4	US-09-711-485-165	Sequence 165, App
87	37	63.8	110	4	US-09-726-219A-248	Sequence 248, App
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89	37	63.8	126	1	US-08-474-040-21	Sequence 21, Appli
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91	37	63.8	126	3	US-08-487-200-21	Sequence 21, Appli
92	37	63.8	126	3	US-08-484-537-21	Sequence 21, Appli
93	37	63.8	213	2	US-08-737-129A-4	Sequence 4, Appli
94	37	63.8	213	2	US-08-737-129A-8	Sequence 8, Appli
95	37	63.8	239	3	US-08-279-772A-4	Sequence 4, Appli
96	37	63.8	239	3	US-08-902-486-11	Sequence 11, Appli
97	37	63.8	599	1	US-08-463-163-31	Sequence 31, Appli
98	36	62.1	661	4	US-09-248-796A-17080	Sequence 8, Appli
99	36	62.1	71	4	US-08-432-694-8	Sequence 8, Appli
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					US-08-308-494A-15	Sequence 15, Appli

ALIGNMENTS

RESULT 1
US-08-230-843-2
Sequence 2, Application US/08230843
Patent No. 5582826
GENERAL INFORMATION:
APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: HAMURO, JUNJI
APPLICANT: NAKAZAWA, HARUMI
APPLICANT: KANAYAMA, YUKA
APPLICANT: SUGAMURA, KAZUO
APPLICANT: TAKESHITA, TOSHIKAZU
TITLE OF INVENTION: IMMUNOSUPPRESSANT
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/230,843
FILING DATE: 21-APR-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 094491/1993
FILING DATE: 21-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 036065/1994
FILING DATE: 07-MAR-1994
FILING DATE: 07-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5582826man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0674-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-230-843-2

Query Match 86.2%; Score 50; DB 1; Length 244;
Best Local Similarity 91.7%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TASSSVSFSYLH 12
|||||
Db 25 TASSSVSSYLH 36

RESULT 2
US-08-636-936-2
Sequence 2, Application US/08636936
Patent No. 5856140
GENERAL INFORMATION:
APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: HAMURO, JUNJI

APPLICANT: NAKAZAWA, HARUMI
APPLICANT: KANAYAMA, YUKA
APPLICANT: SUGAMURA, KAZUO
APPLICANT: TAKESHITA, TOSHIKAZU
TITLE OF INVENTION: IMMUNOSUPPRESSANT
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/636,936
FILING DATE: 24-APR-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/230,843
FILING DATE: 21-APR-1994
APPLICATION NUMBER: JP 094491/1993
FILING DATE: 21-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 036065/1994
FILING DATE: 07-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5856140man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0674-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-636-936-2

Query Match 86.2%; Score 50; DB 2; Length 244;
Best Local Similarity 91.7%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TASSSVSFSYLH 12
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Db 25 TASSSVSSYLH 36

RESULT 3
US-09-563-222C-35
Sequence 35, Application US/09563222C
Patent No. 6696620
GENERAL INFORMATION:
APPLICANT: EPICYTE PHARMACEUTICALS, INC.
APPLICANT: HIATT, ANDREW C.
APPLICANT: HEIN, MICH B.
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
FILE REFERENCE: 068904-0501
CURRENT APPLICATION NUMBER: US/09/563,222C
CURRENT FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: PCT/US01/14349
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/563,222
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 182

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:56:15 ; Search time 69.1875 Seconds
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57.427 Million cell updates/sec

Title: US-10-018-245A-4
Perfect score: 58
Sequence: 1 TASSVSFSYLH 12

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications NA:*
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20: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	50	86.2	108	US-09-842-776A-54	Sequence 54, Appl1
4	47	81.0	109	US-10-818-068-7	Sequence 7, Appl1
5	47	81.0	109	US-10-818-068-8	Sequence 8, Appl1
6	47	81.0	109	US-10-818-068-9	Sequence 9, Appl1
7	47	81.0	109	US-10-818-068-10	Sequence 10, Appl1
8	47	81.0	109	US-10-818-068-11	Sequence 11, Appl1
9	47	81.0	109	US-10-818-068-12	Sequence 12, Appl1
10	47	81.0	109	US-10-724-274-7	Sequence 7, Appl1
11	47	81.0	109	US-10-724-274-8	Sequence 8, Appl1
12	47	81.0	109	US-10-724-274-9	Sequence 9, Appl1
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19	47	81.0	130	US-10-724-274-19	Sequence 19, Appl1
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21	47	81.0	215	US-10-822-000-141	Sequence 141, Appl1
22	47	81.0	215	US-10-724-274-32	Sequence 32, Appl1
23	47	81.0	215	US-10-724-274-33	Sequence 33, Appl1
24	46	79.3	12	US-09-563-222-35	Sequence 35, Appl1
25	46	79.3	12	US-10-783-950-35	Sequence 35, Appl1
26	46	79.3	215	US-10-679-620-120	Sequence 120, Appl1
27	46	79.3	428	US-10-156-761-12746	Sequence 12746, A
28	46	79.3	483	US-10-679-620-122	Sequence 122, Appl1
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31	43	74.1	110	US-10-803-622-256	Sequence 256, Appl1
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33	43	74.1	110	US-10-803-653-256	Sequence 256, Appl1
34	43	74.1	110	US-10-803-653-257	Sequence 257, Appl1
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36	42	72.4	45	US-10-243-130-20	Sequence 20, Appl1
37	42	72.4	45	US-10-243-130-21	Sequence 21, Appl1
38	42	72.4	45	US-10-901-650-20	Sequence 20, Appl1
39	42	72.4	45	US-10-901-650-21	Sequence 21, Appl1
40	42	72.4	109	US-09-144-886-92	Sequence 92, Appl1
41	42	72.4	109	US-09-144-886-97	Sequence 97, Appl1
42	42	72.4	109	US-10-632-706-89	Sequence 89, Appl1
43	42	72.4	109	US-10-632-706-94	Sequence 94, Appl1
44	42	72.4	110	US-10-803-622-238	Sequence 238, Appl1
45	42	72.4	110	US-10-803-622-239	Sequence 239, Appl1
46	42	72.4	110	US-10-803-622-240	Sequence 240, Appl1
47	42	72.4	110	US-10-803-622-241	Sequence 241, Appl1
48	42	72.4	110	US-10-803-622-242	Sequence 242, Appl1
49	42	72.4	110	US-10-803-622-243	Sequence 243, Appl1
50	42	72.4	110	US-10-803-622-244	Sequence 244, Appl1
51	42	72.4	110	US-10-803-622-245	Sequence 245, Appl1
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53	42	72.4	110	US-10-803-653-239	Sequence 239, Appl1
54	42	72.4	110	US-10-803-653-240	Sequence 240, Appl1
55	42	72.4	110	US-10-803-653-241	Sequence 241, Appl1
56	42	72.4	110	US-10-803-653-242	Sequence 242, Appl1
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60	42	72.4	110	US-10-803-653-246	Sequence 246, Appl1
61	42	72.4	110	US-10-803-653-247	Sequence 247, Appl1
62	42	72.4	110	US-10-803-653-248	Sequence 248, Appl1
63	40	69.0	12	US-10-461-885-1	Sequence 1, Appl1
64	40	69.0	12	US-10-461-885-9	Sequence 9, Appl1
65	40	69.0	108	US-10-461-885-14	Sequence 14, Appl1
66	40	69.0	108	US-10-461-885-19	Sequence 19, Appl1
67	40	69.0	108	US-10-461-885-24	Sequence 24, Appl1
68	40	69.0	109	US-10-461-885-29	Sequence 29, Appl1
69	40	69.0	109	US-10-461-885-34	Sequence 34, Appl1
70	40	69.0	109	US-10-461-885-39	Sequence 39, Appl1
71	39	67.2	372	US-10-437-963-177320	Sequence 177320, Appl1
72	38	65.5	57	US-09-144-886-98	Sequence 98, Appl1
73	38	65.5	109	US-09-144-886-99	Sequence 99, Appl1
74	38	65.5	109	US-10-632-706-95	Sequence 95, Appl1
75	38	65.5	160	US-10-081-878-54	Sequence 54, Appl1
76	38	65.5	318	US-09-934-455-90	Sequence 90, Appl1
77	38	65.5	318	US-10-925-066A-524	Sequence 524, Appl1
78	38	65.5	1204	US-10-374-780A-2328	Sequence 2328, Appl1
79	38	65.5	1204	US-10-437-963-188462	Sequence 188462, Appl1
80	37	65.5	1233	US-10-437-963-188462	Sequence 188462, Appl1
81	37	63.8	83	US-10-425-114-44700	Sequence 44700, A
82	37	63.8	83	US-10-468-570-647	Sequence 647, Appl1
83	37	63.8	104	US-10-468-570-647	Sequence 647, Appl1
84	37	63.8	104	US-10-127-890-163	Sequence 163, Appl1
85	37	63.8	106	US-10-127-890-163	Sequence 163, Appl1
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87 37 63.8 106 15 US-10-340-189-83 Sequence 83, Appl
88 37 63.8 106 15 US-10-340-189-84 Sequence 84, Appl
89 37 63.8 106 15 US-10-389-155-1 Sequence 1, Appl
90 37 63.8 106 15 US-10-389-155-27 Sequence 27, Appl
91 37 63.8 106 15 US-10-389-155-28 Sequence 28, Appl
92 37 63.8 106 15 US-10-325-696-49 Sequence 49, Appl
93 37 63.8 106 15 US-10-325-696-51 Sequence 51, Appl
94 37 63.8 106 15 US-10-389-417-1 Sequence 1, Appl
95 37 63.8 106 15 US-10-389-417-27 Sequence 27, Appl
96 37 63.8 106 15 US-10-389-417-28 Sequence 28, Appl
97 37 63.8 106 15 US-10-452-357-1 Sequence 1, Appl
98 37 63.8 106 15 US-10-452-357-7 Sequence 7, Appl
99 37 63.8 106 15 US-10-452-357-8 Sequence 8, Appl
100 37 63.8 106 15 US-10-452-357-16 Sequence 16, Appl

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ALIGNMENTS

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RESULT 1
US-10-018-245A-4
; Sequence 4, Application US/10018245A
; Publication No. US2004015196A1
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, Yoshiaki
; APPLICANT: NAGAHIRA, Kazuhito
; APPLICANT: NAKANISHI, Yoshihiro
; TITLE OF INVENTION: Novel recombinant antibody, amino acid sequences of its complement
; TITLE OF INVENTION: determining regions and genes encoding the same
; FILE REFERENCE: 46224
; CURRENT APPLICATION NUMBER: US/10/018, 245A
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: JP 117394/2000
; PRIOR FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: mouse
; FEATURE:
; OTHER INFORMATION: CDR-L1 of anti-human TNF-alpha antibody
US-10-018-245A-4

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Query Match          100.0%; Score 58; DB 16; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TASSSVSFSYLH 12
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DB 1 TASSSVSFSYLH 12

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RESULT 2
US-09-842-776A-19
; Sequence 19, Application US/09842776A
; Publication No. US20040023316A1
; GENERAL INFORMATION:
; APPLICANT: CONNEX GMBH
; TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS
; TITLE OF INVENTION: IN THE STOOL
; FILE REFERENCE: 41735
; CURRENT APPLICATION NUMBER: US/09/842, 776A
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/EP99/08212
; PRIOR FILING DATE: 1999-10-23
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

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; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Complementarity determining region (CDR1) of an
; OTHER INFORMATION: antibody light chain directed to a 26 kDa-protein
; OTHER INFORMATION: epitope
US-09-842-776A-19

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Query Match          86.2%; Score 50; DB 11; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.031;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 TASSSVSSSYLH 12

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RESULT 3
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; Sequence 54, Application US/09842776A
; Publication No. US20040023316A1
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; APPLICANT: CONNEX GMBH
; TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS
; TITLE OF INVENTION: IN THE STOOL
; FILE REFERENCE: 41735
; CURRENT APPLICATION NUMBER: US/09/842, 776A
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/EP99/08212
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
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; TYPE: PRT
; ORGANISM: Mus musculus
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; Sequence 7, Application US/10818068
; Publication No. US2005002930A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: METHODS OF PRODUCTION AND USE OF ANTI-INTEGRIN ANTIBODIES FOR THE
; TITLE OF INVENTION: CONTROL OF TISSUE GRANULATION
; FILE REFERENCE: 05882.0186.NPUS01
; CURRENT APPLICATION NUMBER: US/10/818, 068
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 41
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; ORGANISM: Homo Sapiens
US-10-818-068-7

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QY 1 TASSSVSFSYLH 12
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DB 24 TASSSVSSNYLH 35

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:54:17 ; Search time 16.875 Seconds
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68.421 Million cell updates/sec

Title: US-10-018-245A-4
Perfect score: 58
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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

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3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	45	77.6	93	2 S17642	Ig kappa chain V r
5	45	77.6	93	2 S17643	Ig kappa chain V r
6	45	77.6	93	2 S17623	Ig kappa chain V r
7	45	77.6	99	2 PH1059	Ig light chain V r
8	45	77.6	99	2 PH1060	Ig light chain V r
9	45	77.6	130	2 B32456	Ig kappa chain pre
10	42	72.4	93	2 S17633	Ig kappa chain V r
11	42	72.4	93	2 S17635	Ig kappa chain V r
12	42	72.4	93	2 S17625	Ig kappa chain V r
13	42	72.4	93	2 S17636	Ig kappa chain V r
14	42	72.4	93	2 S17624	Ig kappa chain V r
15	42	72.4	93	2 S17631	Ig kappa chain V r
16	42	72.4	101	2 S13696	Ig heavy chain V r
17	42	72.4	102	2 S29582	Ig kappa chain V r
18	42	72.4	102	2 S29588	Ig kappa chain V r
19	42	72.4	102	2 S13697	Ig heavy chain V r
20	42	72.4	103	2 S13695	Ig heavy chain V r
21	42	72.4	103	2 S13698	Ig heavy chain V r
22	42	72.4	106	2 S29583	Ig kappa chain V r
23	42	72.4	108	2 PS0069	Ig kappa chain V r
24	42	72.4	109	2 PT0404	Ig light chain V r
25	42	72.4	109	2 PT0405	Ig light chain pre
26	42	72.4	123	2 S05269	Ig kappa chain pre
27	42	72.4	124	2 S05267	Ig kappa chain pre
28	41	70.7	108	2 PS0073	Ig kappa chain V r
29	40	69.0	96	2 C33730	Ig kappa chain V r

30	40	69.0	98	2 PH1061	Ig light chain V r
31	40	69.0	113	2 S03410	Ig kappa chain pre
32	40	69.0	130	2 A32513	Ig kappa chain pre
33	40	69.0	331	2 F72694	hypothetical prote
34	40	69.0	572	2 F77249	hypothetical prote
35	40	69.0	770	2 T50308	probable translati
36	39	67.2	93	2 S17632	Ig kappa chain V r
37	37	63.8	372	2 T31060	hypothetical prote
38	38	65.5	93	2 S17641	Ig kappa chain V r
39	38	65.5	109	2 S13699	Ig kappa chain V r
40	38	65.5	124	2 S20633	Ig kappa chain - h
41	38	65.5	318	2 T00402	homeodomain transc
42	38	65.5	442	2 H86276	F41L7.4 protein -
43	37	63.8	93	2 S17634	Ig kappa chain V r
44	37	63.8	107	2 PD0011	Ig kappa chain V r
45	37	63.8	107	2 PC4405	Ig kappa chain V r
46	37	63.8	200	2 S64905	hypothetical prote
47	37	63.8	365	2 S50409	hypothetical prote
48	37	63.8	450	2 AG1370	glucose-6-phosphat
49	37	63.8	450	2 AE1740	hypothetical prote
50	37	63.8	806	2 T08932	Ig kappa chain V r
51	36	62.1	91	2 S17629	Ig kappa chain V r
52	36	62.1	91	2 S17639	Ig kappa chain V r
53	36	62.1	91	2 S17630	Ig kappa chain V r
54	36	62.1	91	2 S17637	Ig kappa chain V r
55	36	62.1	94	2 S20653	Ig heavy chain V r
56	36	62.1	94	2 S20650	Ig heavy chain V r
57	36	62.1	97	2 S26341	Ig light chain V r
58	36	62.1	97	2 PH1084	Ig light chain V r
59	36	62.1	99	2 D38601	Ig kappa chain V r
60	36	62.1	100	2 S29590	Ig kappa chain V r
61	36	62.1	102	2 S24214	Ig kappa chain - m
62	36	62.1	102	2 S11115	Ig kappa chain V r
63	36	62.1	103	2 S29591	Ig kappa chain V r
64	36	62.1	104	2 B49049	Ig kappa chain V r
65	36	62.1	104	2 JC6076	ant i - D - dimer monoc
66	36	62.1	106	2 PS0071	Ig kappa chain V r
67	36	62.1	106	2 S11114	Ig kappa chain V r
68	36	62.1	106	2 B54378	Ig light chain V r
69	36	62.1	106	2 PS0072	Ig kappa chain V r
70	36	62.1	106	2 S11120	Ig kappa chain V r
71	36	62.1	107	1 KVM5X4	Ig kappa chain V r
72	36	62.1	107	2 S11112	Ig kappa chain V r
73	36	62.1	107	2 S11118	Ig kappa chain V r
74	36	62.1	107	2 S11116	Ig kappa chain V r
75	36	62.1	107	2 S11113	Ig kappa chain V r
76	36	62.1	107	2 PT0401	Ig light chain V r
77	36	62.1	107	2 PT0400	Ig light chain V r
78	36	62.1	107	2 PT0395	Ig light chain V r
79	36	62.1	107	2 PT0402	Ig light chain V r
80	36	62.1	107	2 S11119	Ig kappa chain V r
81	36	62.1	107	2 S11123	Ig kappa chain V r
82	36	62.1	107	2 PT0403	Ig light chain V r
83	36	62.1	107	2 PT0398	Ig light chain V r
84	36	62.1	107	2 S11121	Ig kappa chain V r
85	36	62.1	107	2 S11117	Ig kappa chain V r
86	36	62.1	107	2 PT0399	Ig light chain V r
87	36	62.1	107	2 A30562	Ig kappa chain V r
88	36	62.1	107	2 PT0406	Ig kappa chain V r
89	36	62.1	107	2 B30562	Ig kappa chain V r
90	36	62.1	108	2 G30560	Ig kappa chain V r
91	36	62.1	130	2 JL0079	Ig kappa chain pre
92	36	62.1	140	2 PL0013	Ig kappa chain pre
93	36	62.1	173	2 A71144	hypothetical prote
94	36	62.1	1671	2 S71628	senosy transducti
95	35	60.3	76	2 A48784	Ig kappa V regions
96	35	60.3	93	2 S17640	Ig kappa chain V r
97	35	60.3	108	2 S11125	Ig kappa chain V r
98	35	60.3	130	2 S04573	Ig kappa chain pre
99	35	60.3	167	2 T14620	hypothetical prote
100	35	60.3	261	2 D90123	hypothetical prote

ALIGNMENTS

RESULT 1

PH1058
Ig light chain V region (clone 163.72) - mouse (fragment)

C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: PH1058
R/Title: D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A/Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cells
A/Reference number: PH0871; MUID:92381444; PMID:1512540
A/Accession: PH1058
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-99 <TIL>
A/Cross-references: UNIPROT:Q8K1F1
A/Experimental source: B cell, strain [NZB x NZW]F1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 50; DB 2; Length 99;
Best Local Similarity 91.7%; Pred. No. 0.014; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 1;

Qy 1 TASSVSFSYLH 12
Db 24 TASSVSFSYLH 35

RESULT 2

KVMS7B

Ig kappa chain precursor V region (S107B) - mouse

C/Species: Mus musculus (house mouse)
C/Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 09-Jul-2004
C/Accession: A01943
R/Kwan, S.P.; Max, E.E.; Seidman, J.G.; Leder, P.; Scharff, M.D.
Cell 26, 57-66, 1981
A/Title: Two kappa immunoglobulin genes are expressed in the myeloma S107.
A/Reference number: A01943; MUID:62115300; PMID:6799208
A/Accession: A01943
A/Molecule type: mRNA
A/Residues: 1-129 <KMA>
A/Cross-references: UNIPROT:P01680; GB:V00780; NID:951676; PIDN:CAA24157.1; PID:G51677
A/Note: the sequence was determined from the differentiated gene
C/Comment: This protein, in which there is a deletion of two amino acids at the V-J recombination site, is a kappa chain S107.
C/Genetics: 17/1
A/Intons: 17/1
C/Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16 C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-129/Product: Ig kappa chain V region (S107B) #status predicted <MNT>
F:38-113/Domain: immunoglobulin homology <IMM>
F:45-111/Disulfide bonds: #status predicted

Query Match 79.3%; Score 46; DB 1; Length 129;
Best Local Similarity 83.3%; Pred. No. 0.11; Indels 0; Gaps 0;
Matches 10; Conservative 1; Mismatches 1;

Qy 1 TASSVSFSYLH 12
Db 46 SASSVSFSYLH 57

RESULT 3

S20651

Ig heavy chain V region - mouse
C/Species: Mus musculus (house mouse)

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1995

C/Accession: S20651; S20647
R/Losman, M.; Faasy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A/Description: Relationships among antinuclear antibodies from autoimmune MRL mice react;
A/Reference number: S20639
A/Accession: S20651
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-86 <LOS>
A/Cross-references: EMBL:X65007; NID:952647; PIDN:CAA46140.1; PID:G52648; EMBL:X65010; NID:952648
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin

Query Match 77.6%; Score 45; DB 2; Length 86;
Best Local Similarity 90.9%; Pred. No. 0.11; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1;

Qy 2 ASSVSFSYLH 12
Db 25 ASSVSFSYLH 35

RESULT 4

S17642

Ig kappa chain V region - mouse

C/Species: Mus musculus (house mouse)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C/Accession: S17642
R/Jackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A/Title: Making antibody fragments using phage display libraries.
A/Reference number: S17230; MUID:91326098; PMID:1907718
A/Accession: S17642
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-93 <CLA>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:8-83/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 45; DB 2; Length 93;
Best Local Similarity 90.9%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1;

Qy 2 ASSVSFSYLH 12
Db 17 ASSVSFSYLH 27

RESULT 5

S17643

Ig kappa chain V region - mouse

C/Species: Mus musculus (house mouse)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C/Accession: S17643
R/Jackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A/Title: Making antibody fragments using phage display libraries.
A/Reference number: S17230; MUID:91326098; PMID:1907718
A/Accession: S17643
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-93 <CLA>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:8-83/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 45; DB 2; Length 93;
Best Local Similarity 90.9%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1;

Qy 2 ASSVSFSYLH 12

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:54:17 ; Search time 79.125 Seconds
(without alignments)
77.661 Million cell updates/sec

Title: US-10-018-245A-4
Perfect score: 58
Sequence: 1 TASSSVSFSYLH 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	46	79.3	129 1 KV4A MOUSE	P01680 mus musculus
2	46	79.3	428 1 O82CX6	O82CX6 streptomyc
3	45	77.6	74 2 O8VAB9	O8VAB9 white spot
4	45	77.6	114 2 O8KIF1	O8KIF1 mus musculus
5	42	72.4	101 2 O9JL78	O9JL78 mus musculus
6	40	69.0	131 2 O81IC3	O81IC3 mus musculus
7	40	69.0	331 2 O9YDP9	O9YDP9 aeropyrum p
8	40	69.0	572 2 P73543	P73543 synecocyst
9	40	69.0	770 1 ERG1_SCHPO	ERG1_SCHPO
10	39	67.2	423 2 O6GYK2	O6GYK2 schizosacch
11	38	65.5	218 1 O6Q983	O6Q983 unidentified
12	38	65.5	318 1 AT94_ARATH	AT94_ARATH
13	38	65.5	442 2 O8L8R2	O8L8R2 arabidopsis
14	38	65.5	442 2 O9M9T4	O9M9T4 arabidopsis
15	38	65.5	1204 2 O615B6	O615B6 oryza sativ
16	37	63.8	134 2 O8VDD0	O8VDD0 mus musculus
17	37	63.8	189 2 O6IKM8	O6IKM8 drosophila
18	37	63.8	200 2 O08003	O08003 saccharomyc
19	37	63.8	283 2 O8WSF4	O8WSF4 drosophila
20	37	63.8	283 2 O9VIF7	O9VIF7 drosophila
21	37	63.8	365 1 YH27_YEAST	YH27_YEAST
22	37	63.8	450 1 G6PI_LISTIN	G6PI_LISTIN
23	37	63.8	450 2 G71X61	G71X61 listeria mo
24	37	63.8	450 2 O8XSL0	O8XSL0 listeria s
25	37	63.8	546 2 O7XV72	O7XV72 oryza sativ
26	37	63.8	546 2 O7XV79	O7XV79 oryza sativ
27	37	63.8	739 2 O960P5	O960P5 drosophila
28	37	63.8	806 2 O9SU98	O9SU98 arabidopsis
29	37	63.8	958 2 O6NNB4	O6NNB4 drosophila
30	37	63.8	959 2 O7K5J6	O7K5J6 drosophila
31	37	63.8	959 2 O7K5J6	O7K5J6 drosophila

32	37	63.8	1052 2 O6PCR6	O6PCR6 brachydanio
33	37	63.8	1153 2 O9VFG3	O9VFG3 drosophila
34	36	62.1	107 1 KV6A_MOUSE	KV6A_MOUSE
35	36	62.1	107 1 KV6B_MOUSE	KV6B_MOUSE
36	36	62.1	107 1 KV6C_MOUSE	KV6C_MOUSE
37	36	62.1	107 1 KV6D_MOUSE	KV6D_MOUSE
38	36	62.1	107 1 KV6F_MOUSE	KV6F_MOUSE
39	36	62.1	107 1 KV6G_MOUSE	KV6G_MOUSE
40	36	62.1	107 1 KV6I_MOUSE	KV6I_MOUSE
41	36	62.1	107 1 KV6J_MOUSE	KV6J_MOUSE
42	36	62.1	107 1 KV6L_MOUSE	KV6L_MOUSE
43	36	62.1	112 2 O8K1F0	O8K1F0
44	36	62.1	173 2 O58102	O58102 pyrococcus
45	36	62.1	212 2 O8R538	O8R538 burkholderi
46	36	62.1	215 2 O9AWL3	O9AWL3 oryza sativ
47	36	62.1	269 2 O7RBU2	O7RBU2 plasmodium
48	36	62.1	330 2 O9DSU0	O9DSU0 acovirne d
49	36	62.1	409 2 O7XAA4	O7XAA4 oryza sativ
50	36	62.1	739 2 O8L7F7	O8L7F7 arabidopsis
51	36	62.1	822 2 O6K2K4	O6K2K4 oryza sativ
52	36	62.1	834 2 O8RU34	O8RU34 oryza sativ
53	36	62.1	1670 2 O23901	O23901 dictyosteli
54	36	62.1	1671 2 O869S5	O869S5 dictyosteli
55	35	60.3	127 2 O9N8M6	O9N8M6 trypanosoma
56	35	60.3	136 2 O8LJN1	O8LJN1 oryza sativ
57	35	60.3	139 2 O8MOP2	O8MOP2 anophelies g
58	35	60.3	150 2 O76501	O76501 lytechinus
59	35	60.3	167 2 O40281	O40281 beta vulgar
60	35	60.3	220 2 O81P84	O81P84 drosophila
61	35	60.3	257 2 O9RHU1	O9RHU1 alpha prote
62	35	60.3	257 2 O7CCJ3	O7CCJ3 staphylococ
63	35	60.3	261 2 O98SA2	O98SA2 quillardia
64	35	60.3	289 2 O61G92	O61G92 drosophila
65	35	60.3	307 2 O8RLZ6	O8RLZ6 haemophilus
66	35	60.3	307 2 O7U053	O7U053 haemophilus
67	35	60.3	310 2 O8LJN5	O8LJN5 oryza sativ
68	35	60.3	315 2 O61495	O61495 oryza sativ
69	35	60.3	366 2 O72UN7	O72UN7 leptospira
70	35	60.3	366 2 O8C1X3	O8C1X3 mus musculus
71	35	60.3	394 2 O8F0B7	O8F0B7 leptospira
72	35	60.3	395 1 UNI_PEA	UNI_PEA
73	35	60.3	410 2 O6J728	O6J728 beta vulgar
74	35	60.3	412 1 FNG_DROME	FNG_DROME
75	35	60.3	419 1 G151_HUMAN	G151_HUMAN
76	35	60.3	433 2 O8SUI4	O8SUI4
77	35	60.3	436 2 O82C67	O82C67 streptomyc
78	35	60.3	508 2 O7Q4E3	O7Q4E3 anophelies g
79	35	60.3	518 2 O813Q2	O813Q2 plasmodium
80	35	60.3	536 2 O81F48	O81F48 coxiella bu
81	35	60.3	587 2 O6FLR4	O6FLR4 candida gla
82	35	60.3	608 2 O8A9B1	O8A9B1 bacteroides
83	35	60.3	617 2 O6J740	O6J740 beta vulgar
84	35	60.3	625 2 O6B9X6	O6B9X6 dictyosteli
85	35	60.3	650 2 O74Z59	O74Z59 ashbya goes
86	35	60.3	734 2 O7OYL6	O7OYL6 giardia lam
87	35	60.3	758 2 O815F4	O815F4 plasmodium
88	35	60.3	758 2 O8MS15	O8MS15 plasmodium
89	35	60.3	812 2 O6FPC3	O6FPC3 candida gla
90	35	60.3	885 2 O99SH8	O99SH8 staphylococ
91	35	60.3	885 2 O7A4G3	O7A4G3 staphylococ
92	35	60.3	1041 2 O9DPQ2	O9DPQ2 melegrid h
93	35	60.3	1041 2 O9ELP7	O9ELP7 melegrid h
94	35	60.3	1130 2 O81576	O81576 plasmodium
95	35	60.3	1177 2 O75179	O75179 oryza sativ
96	35	60.3	1292 2 O9ZGE5	O9ZGE5 heliobacilli
97	35	60.3	1573 2 O941S7	O941S7 oryza sativ
98	35	60.3	1710 2 O9V9N7	O9V9N7 drosophila
99	35	60.3	3049 2 O7Q5I8	O7Q5I8 giardia lam
100	34	58.6	108 1 KV6K_MOUSE	KV6K_MOUSE

ALIGNMENTS

```

RESULT 1
KV4A_MOUSE
ID KV4A_MOUSE STANDARD; PRT; 129 AA.
AC P01680;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region S107B precursor.
OS Mus musculus (Mouse)
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Euteleota; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82115300; PubMed=6792308; DOI=10.1016/0092-8674(81)90033-7;
RA Kwan S.-P., Max E.E., Seidman J.G., Leder P., Scharff M.D.;
RT "Two kappa immunoglobulin genes are expressed in the myeloma S107."
RL Cell 26:57-66(1981).
CC -1- MISCELLANEOUS: This protein, in which there is a deletion of two
CC amino acids at the V-J recombination site (after position 118), is
CC synthesized but not secreted in cells that express and secrete the
CC normal kappa chain S107.
CC -----
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CC -----
DR EMBL; J00577; AAA8780.1; -.
DR EMBL; V00780; CAA24157.1; -.
DR PIR; A01943; KMS7B.
DR HSSP; P01679; 2EBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KM Immunoglobulin V region; Signal.
KT SIGNAL
FT CHAIN 1 22
FT DOMAIN 23 129 Ig kappa chain V-IV region S107B.
FT DOMAIN 23 45 Framework-1.
FT DOMAIN 46 57 Complementarity-determining-1.
FT DOMAIN 58 72 Framework-2.
FT DOMAIN 73 79 Complementarity-determining-2.
FT DOMAIN 80 111 Framework-3.
FT DOMAIN 112 118 Complementarity-determining-3.
FT DOMAIN 119 128 Framework-4.
FT DISULFID 45 111 By similarity.
FT NON_TER 129
SQ SEQUENCE 129 AA; 13833 MW; E4AB73072DCFE8B4 CRC64;
Query Match 79.3%; Score 46; DB 1; Length 129;
Best Local Similarity 83.3%; Pred. NO. 0.57;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 TASSSVSFSYLH 12
Db 46 SASSSVSSSYLH 57
RESULT 2
Q82CX6 PRELIMINARY; PRT; 428 AA.
AC Q82CX6;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Putative ROK-family transcriptional regulator.
OS OrderedLocusNames=SAV5212;

```

SX Streptomyces avermitilis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 CC Streptomycineae; Streptomycetaceae; Streptomyces.
 CX NCBI_TaxID=33903;
 RX
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680;
 RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
 RA Omura S., Ikeda H., Ishikawa J., Hamamoto A., Takahashi C.,
 RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
 RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
 RT "genome sequence of an industrial microorganism Streptomyces
 RT avermitilis: deducing the ability of producing secondary
 RT metabolites";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680;
 RX MEDLINE=22608306; PubMed=12692562;
 RA Ikeda H., Ishikawa J., Hamamoto A., Shinose M., Kikuchi H., Shiba T.
 RA Sakaki Y., Hattori M., Omura S.;
 RT "Complete genome sequence and comparative analysis of the industrial
 RT microorganism Streptomyces avermitilis";
 RL Nat. Biotechnol. 21:526-531(2003).
 DR EMBL: AP005042; BAC72924.1; -
 DR InterPro: IPR000600; ROK:
 DR InterPro: IPR009058; WING_hlx_DNA_bnd.
 DR Pfam: PF00480; ROK; 2.
 DR PROSITE: PS01125; ROK; 1.
 KW Complete proteome.
 SQ SEQUENCE 428 AA; 42624 MW; EA489F17A8CBA0FA CRC64;
 QY Query Match 79.3%; Score 46; DB 2; Length 428;
 Db Best Local Similarity 81.8%; Pred. No. 2.1;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps
 2 ASSVSSESYTH 12
 271 ASSSASFAYLH 281
 RESULT 3
 Q8VAB9 PRELIMINARY; PRT; 74 AA.
 ID Q8VAB9
 AC Q8VAB9;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE May506 (WSSV031).
 OS White spot syndrome virus (WSSV).
 OC Viruses; dsRNA viruses, no RNA stage; Nimaviridae; Whispovirus.
 OX NCBI_TaxID=92652;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21548311; PubMed=11689662;
 RX DOI=10.1128/JVI.75.23.11811-11820.2001;
 RA Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.,
 RA Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
 RT "Complete genome sequence of the shrimp white spot bacilliform
 RT virus";
 RL J. Virol. 75:11811-11820(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20517548; PubMed=11062040; DOI=10.1006/viro.2000.0597;
 RA Tsai M.F., Yu H.T., Tzeng H.F., Lwu J.H., Chou C.M., Huang C.J.,
 RA Wang C.H., Lin J.Y., Kou G.H., Lo C.F.;
 RT "identification and characterization of a shrimp white spot syndrome
 RT virus (WSSV) gene that encodes a novel chimeric polypeptide of
 RT cellular-type thymidine kinase and thymidylate kinase";
 RL Virology 277:100-110(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21844071; PubMed=11853398; DOI=10.1006/viro.2001.1273;
 RA Chen L.L., Lwu J.H., Huang C.J., Chou C.M., Chen S.M., Wang C.H.,

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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:54:17 ; Search time 60.75 Seconds
(without alignments)
50,931 Million cell updates/sec

Title: US-10-018-245a-5

Perfect score: 38

Sequence: 1 YSTSNLAS 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database :

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2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	38	100.0	8 5 AAG80315	Aag80315 Anti-huma
2	38	100.0	55 6 ABUS6882	Abus6882 BONT/A Hc
3	38	100.0	55 6 ABUS6871	Abus6871 BONT/A Hc
4	38	100.0	60 6 ABUS6883	Abus6883 BONT/A Hc
5	38	100.0	92 2 AAW89175	Aaw89175 Anti-p53
6	38	100.0	100 2 AAR07319	Aar07319 VK domain
7	38	100.0	100 2 AAW14487	Aaw14487 Monoclonal
8	38	100.0	100 2 AAR9876	Aar9876 Monoclonal
9	38	100.0	102 4 AAB62264	Aab62264 Light cha
10	38	100.0	102 6 AABG72734	Abg72734 Mouse U16
11	38	100.0	105 2 AAW03182	Aaw03182 Guy's 13
12	38	100.0	106 4 AAE13144	Aae13144 Antigen-b
13	38	100.0	106 5 AAU74418	Aau74418 Antigen-b
14	38	100.0	106 6 ABJ26730	Abj26730 VEGF bind
15	38	100.0	106 8 ADK18217	Adk18217 Mouse VEG
16	38	100.0	106 8 ADK18134	Adk18134 Mouse ant
17	38	100.0	106 8 ADK15137	Adk15137 Mouse ant
18	38	100.0	106 8 ADK15136	Adk15136 Mouse ant
19	38	100.0	106 8 ADK15135	Adk15135 Mouse ant
20	38	100.0	107 2 AAW41401	Aaw41401 Humanised
21	38	100.0	107 2 AAW41400	Aaw41400 Humanised
22	38	100.0	107 2 AAW41390	Aaw41390 Anti-CEA
23	38	100.0	107 2 AAW41397	Aaw41397 Anti-CEA
24	38	100.0	107 4 AAB83167	Aab83167 Gangliosid
25	38	100.0	107 4 AAB83159	Aab83159 Mouse gan

26	38	100.0	107 4 AAG63987	Aag63987 Amino aci
27	38	100.0	107 6 ABR40159	AbR40159 Humanised
28	38	100.0	107 8 ADG64762	Adg64762 Cl mouse
29	38	100.0	107 8 ADR38671	Adr38671 Mouse lig
30	38	100.0	107 8 ADR38683	Adr38683 Mouse lig
31	38	100.0	108 2 AAR21294	Aar21294 Murine lig
32	38	100.0	108 2 AAR21290	Aar21290 Murine VL
33	38	100.0	108 2 AAR79884	Aar79884 Anti-EGFR
34	38	100.0	108 2 AAW41388	Aaw41388 Anti-CEA
35	38	100.0	108 3 AAB10021	Aab10021 H. pylori
36	38	100.0	108 3 AAY53591	Aay53591 Light cha
37	38	100.0	108 3 AAY59306	Aay59306 DC8 light
38	38	100.0	108 3 AAY90815	Aay90815 33F8 hydr
39	38	100.0	108 3 AAY97236	Aay97236 Variable
40	38	100.0	108 3 AAB82710	Aab82710 VEGF anta
41	38	100.0	108 5 AAE25956	Aae25956 Mouse ant
42	38	100.0	108 5 AAU74413	Aau74413 Antigen-b
43	38	100.0	108 5 AAG80318	Aag80318 Anti-huma
44	38	100.0	108 6 ABJ26725	Abj26725 VEGF bind
45	38	100.0	108 6 ADE25838	Ade25838 Anti-alpha
46	38	100.0	108 8 ADE25837	Ade25837 Anti-alpha
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48	38	100.0	108 8 ADH59680	Adh59680 Chimeric
49	38	100.0	108 8 ADH59704	Adh59704 PAM4 VK p
50	38	100.0	108 8 ADK18202	Adk18202 Mouse VEG
51	38	100.0	108 8 ADJ25650	Adj25650 Mouse act
52	38	100.0	109 4 AAB81974	Aab81974 Gangliosid
53	38	100.0	109 4 AAB81971	Aab81971 Gangliosid
54	38	100.0	109 5 AAB81278	Aab81278 Murine tr
55	38	100.0	109 6 AABU63531	Aabu63531 Anti-cucu
56	38	100.0	109 6 ADH59678	Adh59678 CPAM4 VK
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64	38	100.0	110 2 AAR21306	Aar21306 Murine VL
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68	38	100.0	110 2 AAR30147	Aar30147 431/26 VK
69	38	100.0	110 8 ADR18144	Adr18144 CAB1 lig
70	38	100.0	110 8 ADJ54097	Adj54097 CAB-1 lig
71	38	100.0	112 8 ADR38684	Adr38684 Mouse lig
72	38	100.0	122 2 AAR25958	Aar25958 ICM-1 in
73	38	100.0	125 4 AAB82702	Aab82702 VEGF anta
74	38	100.0	125 4 AAE13146	Aae13146 Chimeric
75	38	100.0	125 5 AAE28917	Aae28917 c-PI31 v
76	38	100.0	125 5 AAE25966	Aae25966 Mouse ant
77	38	100.0	129 2 AAR53329	Aar53329 KM-796 an
78	38	100.0	129 2 AAY28385	Aay28385 Anti-GM2
79	38	100.0	129 2 AAY28357	Aay28357 Antibody
80	38	100.0	129 8 ADS94357	Ads94357 Antibody
81	38	100.0	130 2 AAW73176	Aaw73176 Light cha
82	38	100.0	130 2 AAW73184	Aaw73184 Fragment
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93	38	100.0	130 2 AAY28381	Aay28381 Human chi
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97	38	100.0	130 2 AAY28380	Aay28380 Human chi
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99 38 100.0 130 2 AAY28382
100 38 100.0 130 8 ADQ31877

AAY28382 Human chi
Adq31877 Antibody

ALIGNMENTS

RESULT 1
AAG80315

ID AAG80315 standard; peptide; 8 AA.

XX AAG80315;

XX 18-FEB-2002 (first entry)

XX Anti-human TNF-alpha CDR-L2 peptide.

XX TNF-alpha; tumour necrosis factor-alpha; antibody; anti-human; CDR;
KM heavy chain; light chain; complementarity determining region; vasotropic;
KM antiarthritic; neuroprotective; protozoacide; toxic shock syndrome;
KM rheumatoid arthritis; malaria; multiple sclerosis.

XX Homo sapiens.

XX WO200179298-A1.

XX 25-OCT-2001.

XX 18-APR-2001; 2001WO-JP003308.

XX 19-APR-2000; 2000JP-00117394.

XX (SUNR) SUNTORY LTD.

XX Fukuda Y, Nagahira K, Nakanishi T;

XX WPI; 2002-066345/09.

XX Novel heavy and light-chain polypeptides of chimeric and humanized
PT antibodies against human tumor necrosis factor alpha for low-
PT immunogenicity treatment of TNF-related diseases such as toxic shock
PT syndrome.

XX Claim 3b; Page 26; 36pp; Japanese.

XX This invention describes novel heavy chain and light chain polypeptides
CC or their fragments of a recombinant antibody to human TNF-alpha which
CC contain complementarity determining region (CDR) sequences. The products
CC of the invention have vasotropic, antiarthritic, neuroprotective and
CC protozoacide activity. The antibodies act by neutralising TNF-alpha in
CC vivo. The antibodies are used for producing chimeric and humanised
CC antibodies that may be used for the treatment and prevention of TNF-alpha
CC associated diseases such as toxic shock syndrome, rheumatoid arthritis,
CC malaria and multiple sclerosis. The antibodies have low immunogenicity in
CC humans. This sequence represents the anti-human tumour necrosis factor-
CC alpha (TNF-alpha) light chain CDR1 designated CDR-L2

XX Sequence 8 AA;

Query Match 100.0%; Score 38; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSTSNLAS 8
|||
Db 1 YSTSNLAS 8

RESULT 2
ABUS6882
ID ABUS6882 standard; protein; 55 AA.
XX
AC ABUS6882;

XX 04-APR-2003 (first entry)

XX BoNT/A Hc binding antibody scfv VL region from 265 #1.

XX Botulinum neurotoxin type A; BoNT/A; mouse; light chain variable region;
KM scfv; antibody; botulism; antibacterial; single chain antibody; VL;
KM immunoglobulin.

XX Mus sp.

XX US2002155114-A1.

XX 24-OCT-2002.

XX 31-AUG-1998; 98US-00144886.

XX 31-AUG-1998; 98US-00144886.

XX (MARK/) MARKS J D.

XX (AMER/) AMERSDORFER P.

XX Marks JD, Amersdorfer P;

XX WPI; 2003-182618/18.

XX Novel antibody that specifically binds and neutralizes botulinum
PT neurotoxin type A useful for neutralizing botulinum neurotoxin and
PT treating botulism.

XX Claim 9; Page 23; 31pp; English.

XX The invention relates to an isolated antibody that specifically binds to
CC an epitope specifically bound by an antibody expressed by a clone such as
CC clone S25, C25, C39, 1C6 and clone 1F3, where the antibody binds to and
CC neutralises botulinum neurotoxin type A (BoNT/A). Also included are a
CC polypeptide comprising BoNT/A neutralising epitope comprising an epitope
CC which is specifically bound by the antibody, where the polypeptide is not
CC a full-length botulinum neurotoxin H₃C fragment and making an anti-BoNT/A
CC antibody that neutralises BoNT/A (by contacting several antibodies with
CC an epitope specifically bound by an antibody expressed by any of the
CC novel clones and isolating an antibody that specifically binds to the
CC epitope). The antibody is useful for neutralising a BoNT/A, by contacting
CC botulinum neurotoxin type A with the antibody comprising VH CDR (heavy
CC chain variable region complementarity determining region) and with a
CC second anti-BoNT/A antibody which comprises a VH CDR, where the second
CC antibody binds to a different epitope than the first anti-BoNT/A
CC antibody. The antibody is useful in the treatment of pathologies
CC associated with botulinum neurotoxin poisoning, for rapid
CC detection/diagnosis of botulism and in the detection and/or
CC quantification of BoNT/A in a biological sample obtained from an organism
CC which is indicative of a Clostridium botulinum infection of the organism.
CC The present sequence is a light chain variable region (VL) of a single
CC chain antibody (scfv) of the invention

XX Sequence 55 AA;

Query Match 100.0%; Score 38; DB 6; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSTSNLAS 8
|||
Db 48 YSTSNLAS 55

RESULT 3
ABUS6871
ID ABUS6871 standard; protein; 55 AA.
XX
AC ABUS6871;
XX
DT 04-APR-2003 (first entry)

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OM protein - protein search, using BW model

Run on: March 24, 2005, 08:57:11 ; Search time 16.125 Seconds
(without alignments)
37.035 Million cell updates/sec

Title: US-10-018-245A-5
Perfect score: 38
Sequence: 1 YSTSNLAS 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	100.0	100	2 US-08-308-494A-15	Sequence 15, Appl
2	38	100.0	105	3 US-08-434-000A-12	Sequence 12, Appl
3	38	100.0	105	3 US-09-312-157-12	Sequence 12, Appl
4	38	100.0	105	4 US-09-717-888-12	Sequence 12, Appl
5	38	100.0	106	4 US-09-798-689-8	Sequence 8, Appl
6	38	100.0	107	3 US-09-171-945-50	Sequence 50, Appl
7	38	100.0	107	3 US-09-171-945-61	Sequence 61, Appl
8	38	100.0	107	3 US-09-171-945-65	Sequence 65, Appl
9	38	100.0	107	3 US-09-171-945-71	Sequence 71, Appl
10	38	100.0	108	3 US-08-483-749A-8	Sequence 8, Appl
11	38	100.0	108	3 US-09-171-945-9	Sequence 9, Appl
12	38	100.0	108	4 US-09-726-219A-244	Sequence 244, Appl
13	38	100.0	109	4 US-09-232-290-7	Sequence 7, Appl
14	38	100.0	110	4 US-09-343-698-8	Sequence 8, Appl
15	38	100.0	110	4 US-08-325-955-8	Sequence 8, Appl
16	38	100.0	110	4 US-09-726-219A-237	Sequence 237, Appl
17	38	100.0	110	4 US-09-726-219A-254	Sequence 254, Appl
18	38	100.0	110	4 US-09-726-219A-255	Sequence 255, Appl
19	38	100.0	110	4 US-09-726-219A-256	Sequence 256, Appl
20	38	100.0	129	2 US-08-116-778E-2	Sequence 2, Appl
21	38	100.0	129	2 US-08-438-562-2	Sequence 2, Appl
22	38	100.0	129	2 US-08-483-528B-92	Sequence 92, Appl
23	38	100.0	130	4 US-09-393-385B-111	Sequence 111, Appl
24	38	100.0	130	4 US-09-393-385B-113	Sequence 113, Appl
25	38	100.0	133	2 US-08-116-778E-37	Sequence 37, Appl
26	38	100.0	133	2 US-08-438-562-37	Sequence 37, Appl
27	38	100.0	133	2 US-08-483-528B-101	Sequence 101, Appl

28	38	100.0	213	3 US-08-630-820-6	Sequence 6, Appl
29	38	100.0	213	4 US-09-273-453-6	Sequence 6, Appl
30	38	100.0	214	4 US-09-653-755A-5	Sequence 5, Appl
31	38	100.0	215	6 5455030-3	Patent No. 5455030
32	38	100.0	215	6 5455030-3	Patent No. 5455030
33	38	100.0	225	6 5455030-5	Patent No. 5455030
34	38	100.0	225	6 5455030-5	Patent No. 5455030
35	38	100.0	235	3 US-09-171-945-17	Sequence 17, Appl
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37	38	100.0	235	3 US-09-171-945-97	Sequence 97, Appl
38	38	100.0	235	3 US-09-171-945-99	Sequence 99, Appl
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44	38	100.0	247	6 5455030-9	Patent No. 5455030
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46	38	100.0	248	6 5455030-11	Patent No. 5455030
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54	38	100.0	666	3 US-09-423-439-51	Sequence 51, Appl
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56	35	92.1	27	3 US-09-344-050-35	Sequence 35, Appl
57	35	92.1	93	3 US-08-783-853A-35	Sequence 35, Appl
58	35	92.1	93	3 US-08-783-853A-66	Sequence 66, Appl
59	35	92.1	93	3 US-09-344-050-35	Sequence 35, Appl
60	35	92.1	97	2 US-09-344-050-66	Sequence 66, Appl
61	35	92.1	97	2 US-08-308-494A-11	Sequence 11, Appl
62	35	92.1	97	3 US-09-280-028-4	Sequence 4, Appl
63	35	92.1	105	1 US-08-211-202-110	Sequence 110, Appl
64	35	92.1	105	1 US-08-459-310-4	Sequence 4, Appl
65	35	92.1	105	4 US-09-091-071-1	Sequence 1, Appl
66	35	92.1	106	1 US-07-634-278-1	Sequence 1, Appl
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69	35	92.1	106	1 US-07-634-278-16	Sequence 16, Appl
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88	35	92.1	106	1 US-08-107-669D-49	Sequence 49, Appl
89	35	92.1	106	1 US-08-107-669D-50	Sequence 50, Appl
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91	35	92.1	106	1 US-08-472-788A-50	Sequence 50, Appl
92	35	92.1	106	1 US-08-472-788A-83	Sequence 83, Appl
93	35	92.1	106	1 US-08-472-788A-84	Sequence 84, Appl
94	35	92.1	106	2 US-08-477-531B-49	Sequence 49, Appl
95	35	92.1	106	2 US-08-477-531B-50	Sequence 50, Appl
96	35	92.1	106	2 US-08-477-531B-51	Sequence 51, Appl
97	35	92.1	106	2 US-08-646-360-163	Sequence 163, Appl
98	35	92.1	106	2 US-08-646-360-164	Sequence 164, Appl
99	35	92.1	106	2 US-08-646-360-165	Sequence 165, Appl
100	35	92.1	106	2 US-08-082-842A-50	Sequence 50, Appl

ALIGNMENTS

```
RESULT 1
US-08-308-494A-15
; Sequence 15, Application US/08308494A
; Patent No. 5959083
; GENERAL INFORMATION:
; APPLICANT: Bossett, Klaus
; APPLICANT: Seeman, Gerhard
; TITLE OF INVENTION: Tetraivalent Bispecific Receptors, The
; TITLE OF INVENTION: Preparation and Use Thereof
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Farnegau, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,494A
; FILING DATE: 21-SEP-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/891,739
; FILING DATE: 01-JUN-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P4118120.4
; FILING DATE: 03-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kulik, David J.
; REGISTRATION NUMBER: 36,576
; REFERENCE/DOCKET NUMBER: 05552-1186-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-308-494A-15

Query Match      100.0%; Score 38; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 YSTSNLAS 8
      |||||
Db      45 YSTSNLAS 52

RESULT 2
US-08-434-000A-12
; Sequence 12, Application US/08434000A
; Patent No. 6046037
; GENERAL INFORMATION:
; APPLICANT: ANDREW C. HIATT, JULIAN
; APPLICANT: K.-C. MA, THOMAS LEHNER
; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
; TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES
```

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NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,000A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application 1
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/367,395
; FILING DATE: 12/30/94
; ATTORNEY/AGENT INFORMATION:
; NAME: Guise, Jeffrey W.
; REGISTRATION NUMBER: 34,613
; REFERENCE/DOCKET NUMBER: 212/127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 552-8400
; TELEFAX: (619) 552-0159
; TELEX: 67-3510
; TELETYPE: SEQUENCE LISTING
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; TOPOLOGY: DESCRIPTION: Guy's 13 Kappa
US-08-434-000A-12

Query Match      100.0%; Score 38; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 1;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 YSTSNLAS 8
      |||||
Db      48 YSTSNLAS 55

RESULT 3
US-09-312-157-12
; Sequence 12, Application US/09312157
; Patent No. 6303341
; GENERAL INFORMATION:
; APPLICANT: ANDREW C. HIATT, JULIAN
; APPLICANT: K.-C. MA, THOMAS LEHNER
; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
; TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:54:17 ; Search time 11.25 seconds
(without alignments)
68.421 Million cell updates/sec

Title: US-10-018-245a-5
Perfect score: 38
Sequence: 1 YSTSNILAS 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

PIR 79: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	91	2	SI7630
2	38	100.0	91	2	SI7626
3	38	100.0	93	2	SI7642
4	38	100.0	93	2	SI7641
5	38	100.0	93	2	SI7640
6	38	100.0	93	2	SI7623
7	38	100.0	96	2	C33730
8	38	100.0	99	2	PH1059
9	38	100.0	99	2	PH1060
10	38	100.0	99	2	PH1058
11	38	100.0	130	2	A32513
12	38	100.0	140	2	PU0013
13	35	92.1	86	2	S20651
14	35	92.1	107	2	A42848
15	34	89.5	67	2	S24216
16	34	89.5	68	2	S26474
17	34	89.5	86	2	S20649
18	34	89.5	86	2	S26459
19	34	89.5	86	2	S29587
20	34	89.5	102	2	S29584
21	34	89.5	104	2	S29592
22	34	89.5	104	2	S26475
23	34	89.5	108	2	S11125
24	34	89.5	108	2	S29581
25	34	89.5	130	2	B32456
26	34	89.5	130	2	S26339
27	33	86.8	90	2	S26339
28	33	86.8	93	2	SI7633
29	33	86.8	93	2	SI7632

30	33	86.8	93	2	SI7635	Ig kappa chain v r
31	33	86.8	93	2	SI7643	Ig kappa chain v r
32	33	86.8	93	2	SI7634	Ig kappa chain v r
33	33	86.8	93	2	SI7636	Ig kappa chain v r
34	33	86.8	93	2	SI7624	Ig kappa chain v r
35	33	86.8	93	2	SI7631	Ig kappa chain v r
36	33	86.8	94	2	S26340	Ig kappa chain v r
37	33	86.8	101	2	SI3696	Ig heavy chain v r
38	33	86.8	102	2	S29582	Ig kappa chain v r
39	33	86.8	102	2	S29588	Ig kappa chain v r
40	33	86.8	102	2	SI3697	Ig heavy chain v r
41	33	86.8	103	2	SI3695	Ig kappa chain v r
42	33	86.8	103	2	SI3698	Ig heavy chain v r
43	33	86.8	105	2	S26338	Ig kappa chain v r
44	33	86.8	106	2	S29583	Ig kappa chain v r
45	33	86.8	108	2	PI0278	Ig kappa chain v r
46	33	86.8	108	2	PI0277	Ig kappa chain v r
47	33	86.8	108	2	PI0276	Ig kappa chain v r
48	33	86.8	108	2	PS0069	Ig kappa chain v r
49	33	86.8	109	2	SI3699	Ig kappa chain v r
50	33	86.8	120	2	S66536	Ig light chain v r
51	33	86.8	123	2	S05269	Ig kappa chain pre
52	33	86.8	124	2	S05267	Ig kappa chain pre
53	32	84.2	94	2	S20653	Ig heavy chain v r
54	32	84.2	94	2	S20650	Ig heavy chain v r
55	32	84.2	106	2	B54378	Ig light chain v r
56	32	84.2	107	2	SI1122	Ig kappa chain v r
57	32	84.2	108	2	S38720	Ig light chain v r
58	32	84.2	113	2	S03410	Ig kappa chain pre
59	32	84.2	129	2	D32513	Ig kappa chain pre
60	32	84.2	1356	2	S51389	ROM2 protein - yea
61	31	81.6	99	2	D38601	Ig kappa chain v r
62	31	81.6	103	2	S73440	hypothetical prote
63	31	81.6	109	2	PT0404	Ig light chain v r
64	31	81.6	109	2	PT0405	Ig light chain v r
65	31	81.6	265	2	AH3513	channel protein nu
66	31	81.6	753	2	S35371	finger protein v r
67	31	81.6	1107	2	S61667	probable membrane
68	30	78.9	138	2	T06173	photosystem II 10X
69	30	78.9	436	2	T22253	hypothetical prote
70	30	78.9	597	2	B82881	hypothetical prote
71	30	78.9	604	2	C85069	hypothetical prote
72	30	78.9	750	2	T42614	probable envelope
73	30	78.9	982	2	A97210	beta galactosidase
74	30	78.9	1466	2	G84516	probable retroelem
75	29	76.3	97	2	PH1085	Ig light chain v r
76	29	76.3	184	2	T28333	ORF MSV172 hypothe
77	29	76.3	198	2	C97638	hypothetical prote
78	29	76.3	198	2	AD2861	hypothetical prote
79	29	76.3	247	2	S66972	probable membrane
80	29	76.3	388	2	S59860	hypothetical prote
81	29	76.3	687	2	S39828	hypothetical prote
82	29	76.3	726	2	T40790	probable permease
83	29	76.3	943	2	JE0121	hypothetical 107.4
84	29	76.3	1046	2	S61610	HPM1 protein - yea
85	29	76.3	1806	2	T23298	hypothetical prote
86	28	73.7	91	2	SI7627	Ig kappa chain v r
87	28	73.7	91	2	SI7629	Ig kappa chain v r
88	28	73.7	91	2	SI7638	Ig kappa chain v r
89	28	73.7	91	2	SI7639	Ig kappa chain v r
90	28	73.7	91	2	SI7628	Ig kappa chain v r
91	28	73.7	91	2	SI7637	Ig kappa chain v r
92	28	73.7	95	2	D33730	Ig kappa chain v r
93	28	73.7	97	2	S26341	Ig light chain v r
94	28	73.7	97	2	PH1084	Ig light chain v r
95	28	73.7	98	2	S26342	Ig kappa chain v r
96	28	73.7	100	2	S29590	Ig kappa chain v r
97	28	73.7	100	2	H33730	Ig kappa chain v r
98	28	73.7	102	2	SI1115	Ig kappa chain v r
99	28	73.7	103	2	S29591	Ig kappa chain v r
100	28	73.7	104	2	JC6076	anti-D-dimer monoc

ALIGNMENTS

RESULT 1

S17630
Ig kappa chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C/Accession: S17630
R/Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A/Title: Making antibody fragments using phage display libraries.
A/Reference number: S17230; PMID:91326098; PMID:1907718
A/Accession: S17630
A/Status: Preliminary
A/Molecule type: nucleic acid
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:8-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSTSNLAS 8
|||||
Db 40 YSTSNLAS 47

RESULT 2

S17626
Ig kappa chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C/Accession: S17626
R/Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A/Title: Making antibody fragments using phage display libraries.
A/Reference number: S17230; PMID:91326098; PMID:1907718
A/Accession: S17626
A/Status: Preliminary
A/Molecule type: nucleic acid
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:8-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSTSNLAS 8
|||||
Db 40 YSTSNLAS 47

RESULT 3

S17642
Ig kappa chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C/Accession: S17642
R/Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A/Title: Making antibody fragments using phage display libraries.
A/Reference number: S17230; PMID:91326098; PMID:1907718
A/Accession: S17642
A/Status: Preliminary
A/Molecule type: nucleic acid
A/Residues: 1-93 <CLA>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

F:8-83/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSTSNLAS 8
|||||
Db 42 YSTSNLAS 49

RESULT 4

S17641
Ig kappa chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C/Accession: S17641
R/Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A/Title: Making antibody fragments using phage display libraries.
A/Reference number: S17230; PMID:91326098; PMID:1907718
A/Accession: S17641
A/Status: Preliminary
A/Molecule type: nucleic acid
A/Residues: 1-93 <CLA>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:8-83/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSTSNLAS 8
|||||
Db 42 YSTSNLAS 49

RESULT 5

S17640
Ig kappa chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C/Accession: S17640
R/Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A/Title: Making antibody fragments using phage display libraries.
A/Reference number: S17230; PMID:91326098; PMID:1907718
A/Accession: S17640
A/Status: Preliminary
A/Molecule type: nucleic acid
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:8-83/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 38; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSTSNLAS 8
|||||
Db 42 YSTSNLAS 49

RESULT 6

S17623
Ig kappa chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C/Accession: S17623
R/Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991

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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:54:17 ; Search time 52.75 Seconds
(without alignments)
77.661 Million cell updates/sec

Title: US-10-018-245A-5
Perfect score: 38
Sequence: 1 YSTSNIAS 8

Scoring table: BLASTSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : UnlProt_03:*
1: unlprot_sprot:*
2: unlprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	112	2	Q8K1F2 mus musculus
2	38	100.0	114	2	Q8K1F1 mus musculus
3	38	100.0	131	2	Q8K1C3 mus musculus
4	35	92.1	97	2	Q9J176 mus musculus
5	35	92.1	253	2	Q8K1C4 plasmodium
6	34	89.5	106	2	Q9U410 schistosoma
7	34	89.5	108	1	KV6K_MOUSE
8	33	86.8	101	2	Q9J178 mus musculus
9	33	86.8	112	2	Q8K1F3 mus musculus
10	32	84.2	940	2	Q6CS17 Kluveromyc
11	32	84.2	1048	2	Q9LBQ9 arthrobacte
12	32	84.2	1051	2	P70745 arthrobacte
13	32	84.2	1266	2	Q6BHV0 debaryomyce
14	32	84.2	1356	1	ROM2_YEAST
15	31	81.6	32	2	Q77UT0 lactate deh
16	31	81.6	32	2	Q9JYP6 lactate deh
17	31	81.6	103	1	YA40_MYCPN
18	31	81.6	265	2	Q8YDZ0 mycoplasma
19	31	81.6	388	2	Q9KIS6 bruceella me
20	31	81.6	391	2	Q9RXP5 bruceella su
21	31	81.6	391	2	Q8RFX6 bruceella su
22	31	81.6	354	2	Q6GIX9 bartonella
23	31	81.6	595	2	Q37901 bacterioph
24	31	81.6	798	2	Q6BV08 debaryomyce
25	31	81.6	849	2	Q6DB45 erwina car
26	31	81.6	1107	2	Q12271 saccharomyc
27	31	81.6	2646	2	Q6XHA6 dictyosteli
28	30	78.9	111	2	Q8L1U6 mus musculu
29	30	78.9	138	1	FSBR_HORVU
30	30	78.9	157	2	Q9M5E0 hordeum vul
31	30	78.9	170	2	Q8S311 medicago sa

32	30	78.9	247	2	Q7V7G5	Q7V7G5 prochloroco
33	30	78.9	325	2	Q9U2Z3	Q9U2Z3 caenorhabdi
34	30	78.9	345	2	Q72FW8	Q72FW8 desulfovibr
35	30	78.9	358	2	Q9PSN1	Q9PSN1 schizosacch
36	30	78.9	375	2	Q94HY4	Q94HY4 oryza sativ
37	30	78.9	375	2	Q7XC54	Q7XC54 oryza sativ
38	30	78.9	379	2	Q7SGV9	Q7SGV9 neurospora
39	30	78.9	420	2	Q20441	Q20441 caenorhabdi
40	30	78.9	431	2	Q6R8B5	Q6R8B5 sodalis glo
41	30	78.9	452	2	Q7V9S4	Q7V9S4 prochloroco
42	30	78.9	479	2	Q7RNF5	Q7RNF5 plasmodium
43	30	78.9	553	2	Q7UER7	Q7UER7 rhodospirill
44	30	78.9	567	2	Q93Q89	Q93Q89 azotobacter
45	30	78.9	597	2	Q9PPX0	Q9PPX0 ureaplasma
46	30	78.9	604	2	Q9S9W0	Q9S9W0 arabidopsis
47	30	78.9	607	2	Q9MAN8	Q9MAN8 arabidopsis
48	30	78.9	624	2	Q9FZ14	Q9FZ14 bacterioph
49	30	78.9	691	2	Q7PZH5	Q7PZH5 anopheles g
50	30	78.9	693	2	Q8RVZ1	Q8RVZ1 arabidopsis
51	30	78.9	698	2	Q8RBJ5	Q8RBJ5 thermoaer
52	30	78.9	703	2	Q8V0L3	Q8V0L3 equid herpe
53	30	78.9	726	2	Q8V0L4	Q8V0L4 equid herpe
54	30	78.9	732	2	Q7XVH8	Q7XVH8 oryza sativ
55	30	78.9	737	2	Q6YU42	Q6YU42 oryza sativ
56	30	78.9	750	2	Q39307	Q39307 equid herpe
57	30	78.9	779	2	Q8V0L2	Q8V0L2 equid herpe
58	30	78.9	804	2	Q8V0L1	Q8V0L1 equid herpe
59	30	78.9	825	2	Q8V0L0	Q8V0L0 equid herpe
60	30	78.9	921	2	Q93F53	Q93F53 cowdria rum
61	30	78.9	982	2	Q97G55	Q97G55 clostridium
62	30	78.9	1063	2	Q8X1B9	Q8X1B9 utillago ma
63	30	78.9	1139	2	Q83BN5	Q83BN5 coxiella bu
64	30	78.9	1466	2	Q9Z0Q3	Q9Z0Q3 arabidopsis
65	30	78.9	3869	2	Q86FQ3	Q86FQ3 cryptospori
66	29	76.3	37	2	Q7QWU7	Q7QWU7 giardia lam
67	29	76.3	106	2	Q9J1X6	Q9J1X6 sulfolobus
68	29	76.3	128	2	Q7VE67	Q7VE67 prochloroco
69	29	76.3	133	2	Q66MD6	Q66MD6 hepatitis c
70	29	76.3	150	2	Q88WQ3	Q88WQ3 lactobacill
71	29	76.3	156	2	Q13536	Q13536 homo sapien
72	29	76.3	173	2	Q7M9K3	Q7M9K3 wolinnella s
73	29	76.3	184	2	Q9YV50	Q9YV50 melanioplus
74	29	76.3	198	2	Q8UD11	Q8UD11 agrobacteri
75	29	76.3	218	2	Q6MTG5	Q6MTG5 mycoplasma
76	29	76.3	301	2	Q6D4Q9	Q6D4Q9 erwina car
77	29	76.3	324	2	Q7QTS2	Q7QTS2 giardia lam
78	29	76.3	291	2	Q720X1	Q720X1 listeria mo
79	29	76.3	301	2	Q6D4Q9	Q6D4Q9 erwina car
80	29	76.3	303	2	Q86196	Q86196 pectobacter
81	29	76.3	324	2	Q7QTS2	Q7QTS2 giardia lam
82	29	76.3	337	2	Q677U4	Q677U4 lymphocyeti
83	29	76.3	345	2	Q87920	Q87920 yersinia in
84	29	76.3	356	2	Q7R882	Q7R882 plasmodium
85	29	76.3	388	2	Q56006	Q56006 sulfolobus
86	29	76.3	405	2	Q6MIV6	Q6MIV6 rhodospirill
87	29	76.3	407	2	Q7UEW9	Q7UEW9 streptococc
88	29	76.3	434	2	Q9ETV8	Q9ETV8 streptococc
89	29	76.3	434	2	Q9EUV8	Q9EUV8 streptococc
90	29	76.3	434	2	Q9F9X2	Q9F9X2 streptococc
91	29	76.3	434	2	Q8E2P6	Q8E2P6 streptococc
92	29	76.3	434	2	Q8E7W4	Q8E7W4 streptococc
93	29	76.3	449	2	Q7S912	Q7S912 neurospora
94	29	76.3	460	2	Q6E612	Q6E612 nosema locu
95	29	76.3	530	2	Q6Z211	Q6Z211 actinoplan
96	29	76.3	605	2	Q88N87	Q88N87 pseudomonas
97	29	76.3	620	2	Q8LLE0	Q8LLE0 solanum tub
98	29	76.3	635	2	Q8A114	Q8A114 bacteroides
99	29	76.3	638	2	Q9XYD8	Q9XYD8 hirtudo medi
100	29	76.3	640	2	Q8T0W4	Q8T0W4 drosophila

ALIGNMENTS

RESULT 1
 Q8K1F2 PRELIMINARY; PRT; 112 AA.
 AC Q8K1F2
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Anti-VIPase light chain variable region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
 RA Zhou Y.-X., Taguchi H., Pianque S., Karle S., Nishiyama Y., Paul S.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF516283; AAM64201.1; -.
 DR PIR; H33932; H33932.
 DR HSSP; P01837; 25C8.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 112
 SQ SEQUENCE 112 AA; 11953 MW; 4716B87FAD8543ED CRC64;

Query Match 100.0%; Score 38; DB 2; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSTSNLAS 8
 |||||
 Db 48 YSTSNLAS 55

RESULT 2
 Q8K1F1 PRELIMINARY; PRT; 114 AA.
 AC Q8K1F1
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Anti-VIPase light chain variable region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
 RA Zhou Y.-X., Taguchi H., Pianque S., Karle S., Nishiyama Y., Paul S.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF516284; AAM64202.1; -.
 DR PIR; A33933; A33933.
 DR PIR; PH1058; PH1058.
 DR HSSP; P01837; 25C8.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 114
 SQ SEQUENCE 114 AA; 12162 MW; 8BD9833DBF3E8FD1 CRC64;

Query Match 100.0%; Score 38; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSTSNLAS 8
 |||||

Db 50 YSTSNLAS 57
 RESULT 3
 Q81IC3 PRELIMINARY; PRT; 131 AA.
 AC Q81IC3
 DT 01-JUN-2003 (TReMBLrel. 24, Created)
 DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Immunoglobulin gamma-3 kappa chain precursor (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MRL/MpJ-Ipr/Ipr; TISSUE=Spleen;
 RX MEDLINE=93156722; PubMed=8429833; DOI=10.1016/0161-5890(93)90089-T;
 RA Takahashi S., Itoh J., Nose M., Ono M., Yamamoto T., Kyogoku M.;
 RT "Cloning and cDNA sequence analysis of nephritic monoclonal
 antibodies derived from an MRL/Ipr lupus mouse."
 RL Mol. Immunol. 30:177-182(1993).
 DR EMBL; D14629; BAA03482.1; -.
 DR HSSP; P01679; 2FBJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 KW signal.
 FT SIGNAL 1 22 Potential.
 FT CHAIN 23 >131 Immunoglobulin gamma-3 kappa chain.
 FT NON_TER 131
 FT NON_TER 131
 SQ SEQUENCE 131 AA; 14083 MW; 5E8365695466E9E CRC64;

Query Match 100.0%; Score 38; DB 2; Length 131;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YSTSNLAS 8
 |||||
 Db 72 YSTSNLAS 79

RESULT 4
 Q9JL76 PRELIMINARY; PRT; 97 AA.
 AC Q9JL76
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Anti-myosin immunoglobulin light chain variable region
 (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DBA/2;
 RX MEDLINE=20446942; PubMed=10992488;
 RX DOI=10.1128/JAI.68.10.5803-5808.2000;
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
 RT "T-Cell-dependent antibody response to the dominant epitope of
 streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
 with cardiac myosin."
 RL Infect. Immun. 68:5803-5808(2000).
 DR EMBL; AF206030; AAF69328.1; -.
 DR HSSP; P01679; 2FBJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:54:17 ; Search time 68.3438 Seconds
(without alignments)
50.931 Million cell updates/sec

Title: US-10-018-245A-6
Perfect score: 52
Sequence: 1 HQYLRSFYT 9

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	9	5	AAG80316 Anti-huma
2	52	100.0	108	5	AAG80318 Anti-huma
3	43	82.7	170	4	AAB88442 Human mem
4	42	80.8	109	8	ADQ31869 Humanised
5	42	80.8	109	8	ADQ31871 Humanised
6	42	80.8	109	8	ADQ31868 Humanised
7	42	80.8	109	8	ADQ31867 Humanised
8	42	80.8	109	8	ADQ31870 Humanised
9	42	80.8	130	8	ADQ31877 Antibody
10	42	80.8	130	8	ADQ31866 Murine an
11	42	80.8	130	8	ADQ31881 Antibody
12	42	80.8	215	8	ADQ31885 Antibody
13	42	80.8	215	8	ADQ31891 Antibody
14	42	80.8	311	4	AAE03721 Murine ch
15	42	80.8	323	4	AAE03723 Murine ma
16	42	80.8	333	4	AAE03720 Murine ch
17	42	80.8	345	4	AAE03732 Murine ch
18	42	80.8	360	4	AAE03723 Rat chond
19	42	80.8	382	4	AAE03722 Rat chond
20	42	80.8	521	6	ADA19155 Rat astro
21	41	78.8	108	3	AAV53591 light cha
22	41	78.8	108	8	ADJ25650 Mouse act
23	41	78.8	129	8	ADJ94357 Antibody
24	40	76.9	112	6	ABJ19266 Anti-huma
25	40	76.9	282	6	ABJ19276 Anti-huma

26	39	75.0	186	8	ADG22610 Cyanophag
27	38	73.1	466	8	ADN24892 Bacterial
28	38	73.1	466	8	ADN22132 Bacterial
29	37	71.2	96	7	ADG42391 SSP doma
30	37	71.2	110	2	AAW46482 StG5 VK a
31	37	71.2	215	8	ADN97547 Artilficia
32	37	71.2	244	2	AAW60780 Fv (GP-2)
33	37	71.2	415	8	ADH22302 ORF2 prot
34	37	71.2	418	7	ADG42373 Chlamydia
35	37	71.2	483	8	ADN97549 Artilficia
36	37	71.2	1136	8	ADN21456 Bacterial
37	37	71.2	1163	8	ADR86509 Aspergill
38	36.5	70.2	388	5	AAW68199 TyLB rela
39	36.5	70.2	388	8	ADM80120 Streptomy
40	36.5	70.2	388	8	ADN97636 S fradiiae
41	36.5	70.2	390	5	AAW68200 TyLB rela
42	36	69.2	156	4	AAW81216 Human hae
43	36	69.2	156	4	AAW65963 Human hep
44	36	69.2	214	4	AAW99905 Human exc
45	36	69.2	214	4	AAW43704 Human bla
46	36	69.2	214	8	ADF71663 Human bla
47	36	69.2	331	5	AAW50383 Human hep
48	36	69.2	439	4	AAU07423 Human hep
49	36	69.2	470	5	AAE18328 Human hep
50	36	69.2	480	4	AAW97634 Human hep
51	36	69.2	480	4	AAU07418 Novel hum
52	36	69.2	480	4	AAW85217 Hepatarnas
53	36	69.2	492	4	AAW84664 Amino aci
54	36	69.2	528	5	AAE18327 Human hep
55	36	69.2	534	4	AAW85216 Hepatarnas
56	36	69.2	534	5	ABP69310 Human pol
57	36	69.2	534	5	AAW50337 Human pre
58	36	69.2	538	4	AAW97633 Human hep
59	36	69.2	582	5	AAE18326 Human hep
60	36	69.2	592	4	AAW97632 Human hep
61	36	69.2	592	4	AAW81062 Human hep
62	36	69.2	592	4	AAU07424 Human hep
63	36	69.2	592	4	AAW85215 Hepatarnas
64	36	69.2	783	8	ADJ25397 Bacterial
65	36	69.2	783	8	ADJ26154 Bacterial
66	36	69.2	783	8	ADJ25671 Bacterial
67	36	69.2	783	8	ADJ22353 Bacterial
68	35	67.3	9	3	AAW10006 H. pylori
69	35	67.3	108	3	AAW10021 H. pylori
70	35	67.3	109	8	ADP03715 Human ant
71	35	67.3	210	3	AAW60307 Arabidops
72	35	67.3	211	3	AAW04495 Arabidops
73	35	67.3	211	3	AAW24847 Arabidops
74	35	67.3	245	3	AAW60306 Arabidops
75	35	67.3	246	3	AAW24846 Arabidops
76	35	67.3	246	3	AAW04494 Arabidops
77	35	67.3	271	3	AAW60305 Arabidops
78	35	67.3	272	3	AAW04493 Arabidops
79	35	67.3	273	3	AAW24845 Arabidops
80	35	67.3	281	8	ADP03813 Human ant
81	35	67.3	310	7	ABO61617 Klebsiell
82	35	67.3	486	6	ABU30698 Protein e
83	35	67.3	506	2	AAW83126 PRTIK48
84	35	67.3	568	4	AAW83126 RNA virus
85	35	67.3	742	2	AAW47232 Cytoomegal
86	35	67.3	899	3	AAW18285 P. gingivi
87	35	67.3	899	3	AAW96029 P. gingivi
88	35	67.3	1732	2	AAW24787 P. gingivi
89	35	67.3	1732	2	AAW24787 P. gingivi
90	34	65.4	9	8	ADH59663 Light cha
91	34	65.4	9	8	ADH59684 Light cha
92	34	65.4	49	4	ABW64277 Drosophil
93	34	65.4	50	4	AAW31159 Peptide #
94	34	65.4	108	7	ADH05266 Female mo
95	34	65.4	108	8	ADH59675 PAM4 VK p
96	34	65.4	108	8	ADH59680 Chimeric
97	34	65.4	108	8	ADH59704 PAM4 VK p
98	34	65.4	108	8	ADM80357 Murine ho

99 34 65.4 109 8 ADH59678
100 34 65.4 109 8 ADH59710

ADH59678 CPAM4 VK
ADH59710 hPAM4 VH

ALIGNMENTS

RESULT 1
AAG80316
ID AAG80316 standard; peptide; 9 AA.

XX
AC AAG80316;

XX
DT 18-FEB-2002 (first entry)

XX
DE Anti-human TNF-alpha CDR-L3 peptide.

XX
KW TNF-alpha; tumour necrosis factor-alpha; antibody; anti-human; CDR;
KW heavy chain; light chain; complementarity determining region; vasotropic;
KW antiarthritic; neuroprotective; protozoacide; toxic shock syndrome;
KW rheumatoid arthritis; malaria; multiple sclerosis.

XX
OS Homo sapiens.

XX
PN WO200179298-A1.

XX
PD 25-OCT-2001.

XX
PF 18-APR-2001; 2001WO-JP003308.

XX
PR 19-APR-2000; 2000JP-00117394.

XX
PA (SUNR) SUNTORY LTD.

XX
PI Fukuda Y, Nagahira K, Nakanishi T;

XX
DR WPI; 2002-066345/09.

XX
PT Novel heavy and light-chain polypeptides of chimeric and humanized
PT antibodies against human tumor necrosis factor alpha for low-
PT immunogenicity treatment of TNF-related diseases such as toxic shock
PT syndrome.

XX
PS Claim 3c; Page 27; 36pp; Japanese.

XX
CC This invention describes novel heavy chain and light chain polypeptides
CC or their fragments of a recombinant antibody to human TNF-alpha which
CC contain complementarity determining region (CDR) sequences. The products
CC of the invention have vasotropic, antiarthritic, neuroprotective and
CC protozoacide activity. The antibodies act by neutralising TNF-alpha in
CC vivo. The antibodies are used for producing chimeric and humanised
CC antibodies that may be used for the treatment and prevention of TNF-alpha
CC associated diseases such as toxic shock syndrome, rheumatoid arthritis,
CC malaria and multiple sclerosis. The antibodies have low immunogenicity in
CC humans. This sequence represents the anti-human tumour necrosis factor-
CC alpha (TNF-alpha) light chain CDR1 designated CDR-L3

XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYLRSPT 9
Db 1 HOYLRSPT 9

RESULT 2
AAG80318
ID AAG80318 standard; protein; 108 AA.
XX
AC AAG80318;

XX
DT 18-FEB-2002 (first entry)

XX
DE Anti-human TNF-alpha L chain CDR region encoding DNA.

XX
KW TNF-alpha; tumour necrosis factor-alpha; antibody; anti-human; CDR;
KW heavy chain; light chain; complementarity determining region; vasotropic;
KW antiarthritic; neuroprotective; protozoacide; toxic shock syndrome;
KW rheumatoid arthritis; malaria; multiple sclerosis.

XX
OS Homo sapiens.

XX
PN WO200179298-A1.

XX
PD 25-OCT-2001.

XX
PF 18-APR-2001; 2001WO-JP003308.

XX
PR 19-APR-2000; 2000JP-00117394.

XX
PA (SUNR) SUNTORY LTD.

XX
PI Fukuda Y, Nagahira K, Nakanishi T;

XX
DR WPI; 2002-066345/09.

XX
DR N-PSDB; AAI69376.

XX
PT Novel heavy and light-chain polypeptides of chimeric and humanized
PT antibodies against human tumor necrosis factor alpha for low-
PT immunogenicity treatment of TNF-related diseases such as toxic shock
PT syndrome.

XX
PS Disclosure; Page 28-29; 36pp; Japanese.

XX
CC This invention describes novel heavy chain and light chain polypeptides
CC or their fragments of a recombinant antibody to human TNF-alpha which
CC contain complementarity determining region (CDR) sequences. The products
CC of the invention have vasotropic, antiarthritic, neuroprotective and
CC protozoacide activity. The antibodies act by neutralising TNF-alpha in
CC vivo. The antibodies are used for producing chimeric and humanised
CC antibodies that may be used for the treatment and prevention of TNF-alpha
CC associated diseases such as toxic shock syndrome, rheumatoid arthritis,
CC malaria and multiple sclerosis. The antibodies have low immunogenicity in
CC humans. This sequence represents the anti-human tumour necrosis factor-
CC alpha (TNF-alpha) light chain CDR fragment described in the invention

XX
SQ Sequence 108 AA;

Query Match 100.0%; Score 52; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HOYLRSPT 9
Db 90 HOYLRSPT 98

RESULT 3
AAB88442
ID AAB88442 standard; protein; 170 AA.

XX
AC AAB88442;

XX
DT 23-MAY-2001 (first entry)

XX
DE Human membrane or secretory protein clone PSEC0224.

XX
KW Human; secretory protein; membrane protein; vaccine; gene therapy;
KW rheumatoid arthritis; diabetes.

XX
OS Homo sapiens.

XX
PN EPI067182-A2.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:57:11 ; Search time 18.1406 Seconds
(without alignments)
37.035 Million cell updates/sec

Title: US-10-018-245A-6

Perfect score: 52

Sequence: 1 HQYLRSPYR 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PTCUS_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	71.2	231	1	US-08-681-432-1
2	37	71.2	244	1	US-08-230-843-2
3	37	71.2	244	2	US-08-636-936-2
4	35	67.3	310	4	US-09-489-039A-8134
5	35	67.3	1732	2	US-08-570-311-10
6	35	67.3	1732	2	US-08-353-485-10
7	35	67.3	1732	4	US-09-066-330-11
8	34	65.4	55	4	US-09-270-767-4677
9	34	65.4	55	4	US-09-270-767-49894
10	34	65.4	114	4	US-09-248-796A-23592
11	34	65.4	213	3	US-09-540-236-2378
12	34	65.4	278	3	US-09-134-001C-3651
13	34	65.4	367	2	US-08-655-704B-17
14	34	65.4	367	3	US-09-107-755-17
15	34	65.4	605	4	US-09-253-991A-25512
16	34	65.4	660	4	US-09-198-452A-578
17	34	65.4	947	4	US-09-377-850-3
18	34	65.4	956	4	US-09-438-185A-541
19	33	63.5	20	4	US-09-690-454-120
20	33	63.5	92	2	US-08-273-146-45
21	33	63.5	92	2	US-08-273-146-53
22	33	63.5	134	3	US-09-540-236-3720
23	33	63.5	145	3	US-09-096-244-2
24	33	63.5	175	4	US-09-710-279-1874
25	33	63.5	188	4	US-09-248-796A-21795
26	33	63.5	195	4	US-09-173-300-42
27	33	63.5	195	4	US-10-027-450-42

28	33	63.5	217	4	US-09-690-454-112	Sequence 112, App
29	33	63.5	276	4	US-09-719-402A-6	Sequence 6, Appli
30	33	63.5	323	4	US-09-902-540-15597	Sequence 15597, A
31	33	63.5	391	4	US-09-543-681A-5945	Sequence 5945, Ap
32	33	63.5	428	4	US-09-173-300-36	Sequence 36, Appl
33	33	63.5	428	4	US-10-027-450-36	Sequence 36, Appl
34	33	63.5	443	4	US-09-173-300-38	Sequence 38, Appl
35	33	63.5	443	4	US-10-027-450-38	Sequence 38, Appl
36	33	63.5	539	4	US-09-719-402A-2	Sequence 2, Appli
37	33	63.5	738	4	US-09-252-991A-27291	Sequence 27291, A
38	33	63.5	922	4	US-09-345-236B-89	Sequence 89, Appl
39	33	63.5	1335	3	US-09-134-001C-3716	Sequence 3716, Ap
40	33	63.5	3177	2	US-08-477-451-4	Sequence 4, Appli
41	32.5	62.5	3472	4	US-09-408-020-4	Sequence 4, Appli
42	32	61.5	128	4	US-09-225-322B-10	Sequence 19, Appl
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100	31	59.6	518	3	PCT-US95-06770-8	Sequence 7, Appli
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					US-09-113-309-19	

ALIGNMENTS

RESULT 1
US-08-681-432-1
Sequence 1, Application US/08681432
Patent No. 5800991
GENERAL INFORMATION:
APPLICANT: HALEY, Boyd E.
APPLICANT: KOHLER, Heinz
APPLICANT: RAJAGOPALAN, Krishnan
APPLICANT: PAVLINKOVA, Gabriela
TITLE OF INVENTION: NUCLEOTIDE OR NUCLEOSIDE PHOTOAFFINITY
TITLE OF INVENTION: COMPOUND MODIFIED ANTIBODIES, METHODS FOR THEIR
TITLE OF INVENTION: MANUFACTURE AND USE THEREOF AS DIAGNOSTICS AND
TITLE OF INVENTION: THERAPEUTICS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURN, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/681,432
FILING DATE: 23-JUL-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/208,822
FILING DATE: 11-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 028750-132
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-681-432-1

Query Match 71.2%; Score 37; DB 1; Length 231;
Best Local Similarity 77.8%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYLRSPYT 9
Db 90 HOYHRSPLT 98

RESULT 2
US-08-230-843-2
Sequence 2, Application US/08230843
Patent No. 5582826
GENERAL INFORMATION:
APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: HAMURO, JUNJI
APPLICANT: NAKAZAWA, HARUMI
APPLICANT: KANAYAMA, YUKA
APPLICANT: SUGAMURA, KAZUO

APPLICANT: TAKESHITA, TOSHIKAZU
TITLE OF INVENTION: IMMUNOSUPPRESSANT
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/230,843
FILING DATE: 21-APR-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 094491/1993
FILING DATE: 21-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 036065/1994
FILING DATE: 07-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5582826man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0674-0X
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-230-843-2

Query Match 71.2%; Score 37; DB 1; Length 244;
Best Local Similarity 77.8%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYLRSPYT 9
Db 91 HOYHRSPLT 99

RESULT 3
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Sequence 2, Application US/08636936
Patent No. 5856140
GENERAL INFORMATION:
APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: HAMURO, JUNJI
APPLICANT: NAKAZAWA, HARUMI
APPLICANT: KANAYAMA, YUKA
APPLICANT: SUGAMURA, KAZUO
APPLICANT: TAKESHITA, TOSHIKAZU
TITLE OF INVENTION: IMMUNOSUPPRESSANT
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:56:15 ; Search time 51.8906 Seconds
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Title: US-10-018-245A-6
Perfect score: 52
Sequence: 1 HOYLRSPYR 9

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Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
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Listing first 100 summaries

Database :

Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	42	80.8	109	16	US-10-818-068-11
7	42	80.8	109	16	US-10-818-068-12
8	42	80.8	109	16	US-10-724-274-7
9	42	80.8	109	17	US-10-724-274-8
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27	37	71.2	215	16	US-10-679-620-120	Sequence 120, Appl
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46	36	69.2	214	14	US-10-080-254-98	Sequence 98, Appl
47	36	69.2	214	15	US-10-242-355-642	Sequence 642, Appl
48	36	69.2	439	9	US-09-978-249-12	Sequence 12, Appl
49	36	69.2	480	9	US-09-978-249-7	Sequence 7, Appl
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52	36	69.2	534	9	US-09-836-461-2	Sequence 2, Appl
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68	35	67.3	486	15	US-10-282-122A-58622	Sequence 58622, A
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74	34	65.4	50	9	US-09-864-761-48732	Sequence 48732, A
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76	34	65.4	108	15	US-10-461-878-14	Sequence 14, Appl
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80	34	65.4	109	17	US-10-461-885-16	Sequence 16, Appl
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84	34	65.4	239	16	US-10-437-963-125614	Sequence 125614, Appl
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91	34	65.4	660	15	US-10-289-762-578	Sequence 578, App
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94	34	65.4	854	15	US-10-170-385-59	Sequence 59, Appl
95	34	65.4	1087	15	US-10-369-493-6801	Sequence 6801, Ap
96	34	65.4	1564	9	US-09-801-368-244	Sequence 244, App
97	34	65.4	1564	15	US-10-369-493-22424	Sequence 22424, A
98	33	63.5	9	9	US-09-861-294-10	Sequence 10, Appl
99	33	63.5	9	9	US-09-924-099-5	Sequence 5, Appl
100	33	63.5	9	14	US-10-367-506-10	Sequence 10, Appl

ALIGNMENTS

```

RESULT 1
; Sequence 6, Application US/10018245A
; Publication No. US2004015196A1
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, Yoshiaki
; APPLICANT: NAGAHIRA, Kazuhiro
; APPLICANT: NAKAMISHI, Toshihiro
; TITLE OF INVENTION: Novel recombinant antibody, amino acid sequences of its complement
; TITLE OF INVENTION: determining regions and genes encoding the same
; FILE REFERENCE: 46224
; CURRENT APPLICATION NUMBER: US/10/018,245A
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: JP 117394/2000
; PRIOR FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: mouse
; FEATURE:
; OTHER INFORMATION: CDR-L3 of anti-human TNF-alpha antibody
US-10-018-245A-6

Query Match
Best Local Similarity 100.0%; Score 52; DB 16; Length 9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 HOYLRSPYT 9

RESULT 2
US-10-818-068-7
; Sequence 7, Application US/10818068
; Publication No. US20050002930A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: METHODS OF PRODUCTION AND USE OF ANTI-INTEGRIN ANTIBODIES FOR THE
; TITLE OF INVENTION: CONTROL OF TISSUE GRANULATION
; FILE REFERENCE: 05882.0186.NPUS01
; CURRENT APPLICATION NUMBER: US/10/818,068
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
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; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-818-068-7

Query Match
Best Local Similarity 80.8%; Score 42; DB 16; Length 109;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLRSPYT 9
DB 90 HOYLRSPYT 98

RESULT 3
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; Sequence 8, Application US/10818068
; Publication No. US20050002930A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: METHODS OF PRODUCTION AND USE OF ANTI-INTEGRIN ANTIBODIES FOR THE
; TITLE OF INVENTION: CONTROL OF TISSUE GRANULATION
; FILE REFERENCE: 05882.0186.NPUS01
; CURRENT APPLICATION NUMBER: US/10/818,068
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
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; LENGTH: 109
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; ORGANISM: Homo Sapiens
US-10-818-068-8

Query Match
Best Local Similarity 80.8%; Score 42; DB 16; Length 109;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLRSPYT 9
DB 90 HOYLRSPYT 98

RESULT 4
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; Sequence 9, Application US/10818068
; Publication No. US20050002930A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: METHODS OF PRODUCTION AND USE OF ANTI-INTEGRIN ANTIBODIES FOR THE
; TITLE OF INVENTION: CONTROL OF TISSUE GRANULATION
; FILE REFERENCE: 05882.0186.NPUS01
; CURRENT APPLICATION NUMBER: US/10/818,068
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-818-068-9

Query Match
Best Local Similarity 80.8%; Score 42; DB 16; Length 109;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLRSPYT 9
DB 90 HOYLRSPYT 98

RESULT 5
US-10-818-068-10
; Sequence 10, Application US/10818068
; Publication No. US20050002930A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: METHODS OF PRODUCTION AND USE OF ANTI-INTEGRIN ANTIBODIES FOR THE
; TITLE OF INVENTION: CONTROL OF TISSUE GRANULATION
; FILE REFERENCE: 05882.0186.NPUS01
US-10-818-068-10

Query Match
Best Local Similarity 80.8%; Score 42; DB 16; Length 109;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLRSPYT 9
DB 90 HOYLRSPYT 98

```


ALIGNMENTS

RESULT 1

S61665

probable membrane protein YOR107w - yeast (Saccharomyces cerevisiae)

N/Alternate names: hypothetical protein O3224; hypothetical protein YOR3224w
C/Species: Saccharomyces cerevisiae
C/Date: 09-Mar-1996 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C/Accession: S61665; S66992R/Benes, V.; Andrade, M.A.; Rechmann, S.; Teodoru, C.; Banreyl, A.; Sander, C.; Valencia
submitted to the EMBL Data Library, December 1995A/Description: Nucleotide sequence and analysis of a 130 kb fragment of yeast chromosome
A/Reference number: S61643

A/Accession: S61665

A/Molecule type: DNA

A/Residues: 1-309 <BEN>

A/Cross-references: UNIPROT:Q99188; EMBL:X94335; NID:g1262139; PID:e217829; PID:g164952
R/Voss, H.; Benes, V.; Rechmann, S.; Teodoru, C.; Schwager, C.; Paces, V.; Ansoorge, W.
submitted to the Protein Sequence Database, July 1996

A/Reference number: S66965

A/Accession: S66992

A/Molecule type: DNA

A/Residues: 1-309 <VOS>

A/Cross-references: EMBL:Z75015; NID:g1420290; PID:e252009; PID:g1420291; MIPS:YOR107w
A/Experimental source: strain S288C

C/Genetics:

A/Gene: SGD:RGS2

A/Cross-references: SGD:S0005633

A/Map position: 15R

C/Superfamily: Saccharomyces cerevisiae probable membrane protein YOR107w
C/Keywords: transmembrane protein

F/129-145/Domain: transmembrane #status predicted <TMM>

Query Match 73.1%; Score 38; DB 2; Length 309;

Best Local Similarity 66.7%; Pred. No. 8.9;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLRSPYT 9

Db 39 HERMRSPYT 47

RESULT 2

PH1059

Ig light chain V region (clone 17s-cl) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C/Accession: PH1059R/Tillman, D.W.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992A/Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
A/Reference number: PH0971; MUID:92381444; PMID:1512540

A/Accession: PH1059

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-99 <TIL>

A/Experimental source: B cell, strain [NZB x NZW]F1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: immunoglobulin

F/16-91/Domain: immunoglobulin homology <IMM>

Query Match 71.2%; Score 37; DB 2; Length 99;

Best Local Similarity 77.8%; Pred. No. 4.1;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYLRSPYT 9

Db 90 HOYHRSPYT 98

RESULT 3

S46373

Ig kappa chain V-J region (T24-9) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C/Accession: S46373; S38647R/Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994A/Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rear
A/Reference number: S46369; MUID:94313975; PMID:8039491

A/Accession: S46373

A/Molecule type: mRNA

A/Residues: 1-132 <BEN>

A/Cross-references: EMBL:Z27174; NID:g415963; PIDN:CAA81698.1; PID:g415964

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/34-114/Domain: immunoglobulin homology <IMM>

Query Match 71.2%; Score 37; DB 2; Length 132;

Best Local Similarity 66.7%; Pred. No. 5.6;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYLRSPYT 9

Db 113 HOYSSPFT 121

RESULT 4

D71460

probable membrane thiol proteinase - Chlamydia trachomatis (serotype D, strain UW3/Cx)

C/Species: Chlamydia trachomatis

C/Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C/Accession: D71460R/Stephens, R.S.; Kaiman, S.; Lammel, C.J.; Pan, J.; Marache, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998A/Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tract
A/Reference number: A71570; MUID:9900809; PMID:9784136

A/Accession: D71460

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-418 <ARN>

A/Cross-references: UNIPROT:O84876; GB:AE001360; GB:AE001273; NID:g3329342; PIDN:AAC68466

A/Experimental source: serotype D, strain UW-3/Cx

C/Genetics:

A/Gene: CT868

Query Match 71.2%; Score 37; DB 2; Length 418;

Best Local Similarity 66.7%; Pred. No. 19;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HOYLRSPYT 9

Db 367 HWYLRDPFT 375

RESULT 5

JQ1744

hypothetical 77.2K protein - rabbit fibroma virus

N/Alternate names: H3r protein

C/Species: rabbit fibroma virus, Shope fibroma virus

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: JQ1744R/Masung, R.F.; McFadden, G.; Moyer, R.W.
J. Gen. Virol. 73, 2903-2911, 1992

A/Title: Nucleotide sequence analysis of a unique near-terminal region of the tumorigenic

A/Reference number: JQ1741; MUID:93057362; PMID:1331293

A/Accession: JQ1744

A/Molecule type: DNA

A/Residues: 1-673 <MAS>

A/Cross-references: UNIPROT:Q9G8T5

Query Match 71.2%; Score 37; DB 2; Length 673;

Best Local Similarity 75.0%; Pred. No. 33;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 08:54:17 ; Search time 59.3438 Seconds
(without alignments)
77.661 Million cell updates/sec

Title: US-10-018-245A-6
Perfect score: 52
Sequence: 1 HQYLRSPYR 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : UniProt 03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	82.7	170	2	O8N2E2
2	43	82.7	565	2	O7MEIO
3	42	80.8	333	2	O6NXYO
4	42	80.8	447	1	CRDL_MOUSE
5	42	80.8	521	2	O76LDO
6	41	78.8	234	1	NPD_IACPL
7	39	75.0	909	2	O7JPB1
8	39	75.0	911	2	O7JPB0
9	38	73.1	88	2	O49251
10	38	73.1	197	2	O92439
11	38	73.1	289	2	O7V6U4
12	38	73.1	309	2	O99188
13	38	73.1	336	1	RT09_CANAL
14	38	73.1	403	2	O99RUT8
15	38	73.1	496	2	O81JF7
16	38	73.1	760	2	O8BXL8
17	37	71.2	168	2	O69LW6
18	37	71.2	418	2	O84876
19	37	71.2	446	2	O6A078
20	37	71.2	488	2	O91GHI
21	37	71.2	588	2	O82G94
22	37	71.2	626	2	O8RUR0
23	37	71.2	635	2	O6CDF3
24	37	71.2	635	2	O6CH21
25	37	71.2	639	2	O6C1X7
26	37	71.2	673	2	O908T5
27	37	71.2	675	2	O908R6
28	37	71.2	916	2	O6K1V9
29	37	71.2	1089	2	O6C3L8
30	37	71.2	1111	1	SEC8_NEUCR
31	37	71.2	1171	2	O7YXU7

32	37	71.2	1794	2	O9S168	O9e168 arabidopsis
33	36.5	70.2	388	2	O54142	O54142 streptomyc
34	36	69.2	322	2	O17066	O17066 caenorhabd
35	36	69.2	363	2	O07544	O07544 bacillus su
36	36	69.2	480	2	O9HB39	O9hb39 homo sapien
37	36	69.2	484	1	Y330_SHEON	O6ejx6 shewanella
38	36	69.2	514	2	O8WM03	O8wm03 oryza sativ
39	36	69.2	534	2	O9HB38	O9hb38 homo sapien
40	36	69.2	548	2	O8WMQ1	O8wmq1 homo sapien
41	36	69.2	592	2	O8WMQ2	O8wmq2 homo sapien
42	36	69.2	592	2	O9HB37	O9hb37 homo sapien
43	36	69.2	693	2	O8GVZ1	O8gvz1 oryza sativ
44	36	69.2	778	2	O8U8E7	O8u8e7 agrobacteri
45	36	69.2	916	2	O8RX35	O8rx35 arabidopsis
46	36	69.2	931	2	O04026	O04026 arabidopsis
47	36	69.2	936	2	O04025	O04025 arabidopsis
48	35	67.3	89	2	O48636	O48636 alstroemer
49	35	67.3	91	2	O9N3P7	O9n3p7 caenorhabd
50	35	67.3	165	2	O6K652	O6k652 oryza sativ
51	35	67.3	246	2	O818T7	O818t7 arabidopsis
52	35	67.3	251	2	O9FMW9	O9fmm9 arabidopsis
53	35	67.3	345	2	O56F06	O56f06 vibrio chol
54	35	67.3	486	1	THRC_HELPJ	O56605 vibrio chol
55	35	67.3	486	1	THRC_HELPY	O9amx5 helicobacte
56	35	67.3	538	2	O86030	O24924 helicobacte
57	35	67.3	598	2	O8B0U3	O86030 vibrio chol
58	35	67.3	609	2	O8A532	O860u3 helicobasid
59	35	67.3	641	2	O52824	O8a532 bacteroides
60	35	67.3	641	2	O9FDG2	O52824 rhizobium l
61	35	67.3	663	1	SEPI_SCHPO	O9fdg2 rhizobium e
62	35	67.3	705	2	O87192	O43058 schizosach
63	35	67.3	718	2	O7R011	O87192 vibrio para
64	35	67.3	818	1	COLA_VIBCH	O7r011 plasmodium
65	35	67.3	899	2	O96237	O9crj0 vibrio chol
66	35	67.3	906	2	O7R6M5	O96237 plasmodium
67	35	67.3	1040	2	O7Q614	O7rbm5 plasmodium
68	35	67.3	1358	2	O6Q474	O7q614 amophles g
69	35	67.3	1732	2	O07442	O6q474 porphyromon
70	35	67.3	1732	2	O52050	O07442 porphyromon
71	35	67.3	1732	2	O51817	O52050 porphyromon
72	35	67.3	3901	2	O9N533	O51817 porphyromon
73	34	65.4	89	2	O49240	O9n533 caenorhabd
74	34	65.4	101	2	O7MLR5	O49240 alstroemer
75	34	65.4	136	2	O8HP94	O7mlr5 bordetella
76	34	65.4	136	2	O8HPB7	O8hp94 ciindela r
77	34	65.4	140	2	O94TP6	O8hp7 ciindela c
78	34	65.4	143	2	O8HP95	O94tp6 ciindela c
79	34	65.4	159	2	O8HP81	O8hp95 ciindela m
80	34	65.4	161	2	O94TP4	O8hp81 ciindela b
81	34	65.4	162	2	O94TK3	O94tp4 ciindela m
82	34	65.4	162	2	O94TK5	O94tk3 pentacomia
83	34	65.4	162	2	O94TK7	O94tk5 ciindela u
84	34	65.4	162	2	O94TL1	O94tk7 ciindela c
85	34	65.4	162	2	O94TL4	O94tl1 ciindela d
86	34	65.4	162	2	O94TP5	O94tl4 ciindela p
87	34	65.4	162	2	O94TP7	O94tp5 ciindela b
88	34	65.4	162	2	O94TP8	O94tp7 ciindela a
89	34	65.4	162	2	O94TP9	O94tp8 ciindela t
90	34	65.4	162	2	O94TQ0	O94tp9 ciindela d
91	34	65.4	162	2	O94TQ1	O94tq0 ciindela i
92	34	65.4	162	2	O94TQ2	O94tq1 ciindela o
93	34	65.4	162	2	O8HP75	O94tq2 ciindela d
94	34	65.4	162	2	O8HP75	O8hp75 ciindela n
95	34	65.4	162	2	O8HP89	O8hp75 ciindela c
96	34	65.4	162	2	O8HP90	O8hp89 ciindela c
97	34	65.4	162	2	O8HP96	O8hp90 ciindela v
98	34	65.4	162	2	O8HP97	O8hp96 ciindela t
99	34	65.4	162	2	O8HPA2	O8hp97 ciindela s
100	34	65.4	162	2	O8HPB0	O8hpa2 ciindela r
						O8hpb0 ciindela o

ALIGNMENTS

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RESULT 1
Q8N2E2 ID Q8N2E2 PRELIMINARY; PRT; 170 AA.
AC Q8N2E2;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE Hypothetical protein PSEC0224.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole embryo;
RA Oca T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
RA Saito K., Yamamoto J., Makamatsu A., Nagai T., Nakamura Y.,
RA Nagahari K., Sugano S., Isogai T.,
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075525; BAC11671.1;
SQ SEQUENCE 170 AA; 18999 MW; 38EP957175E50D73 CRC64;

Query March 82.7%; Score 43; DB 2; Length 170;
Best Local Similarity 87.5%; Pred. No. 2.2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HOYLRSPPY 8
Db 28 HQFLRSPY 35

RESULT 2
Q7MEIO ID Q7MEIO PRELIMINARY; PRT; 565 AA.
AC Q7MEIO;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DE Hypothetical protein VVA0690.
OS OrderedLocustNames=VVA0690;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=196600;
RN [1]
RP SEQUENCE FROM N.A.
RA PubMed=14656965; DOI=10.1101/gr.1295503;
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
RA Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
RA Shao C.-P., Lee C.-T., Hor L.-J., Tsai S.-F.;
RT "Comparative genome analysis of Vibrio vulnificus, a marine
RT pathogen."
RL Genome Res. 13:2577-2587(2003).
DR EMBL; AP005347; BAC96716.1;
DR InterPro; IPR002789; DUF87.
DR Pfam; PF01935; DUF87.1.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 565 AA; 62426 MW; 478F1601A7F1E98E CRC64;

Query March 82.7%; Score 43; DB 2; Length 565;
Best Local Similarity 87.5%; Pred. No. 8.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Chrd11 protein.
GN Name=Chrd11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD1; TISSUE=Neural Stem Cell;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stepien M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uebin T.B., Toshimuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CD1; TISSUE=Neural Stem Cell;
RA Strausberg R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC066832; AAH66832.1;
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR01007; VWF_C.
DR Pfam; PF00093; VMC_3.
DR SMART; SM00214; VMC_3.
DR PROSITE; PS01208; VWF_C_1; 3.
DR PROSITE; PS50184; VWF_C_2; 3.
SQ SEQUENCE 333 AA; 37035 MW; A82093A24174E1D6 CRC64;

Query March 80.8%; Score 42; DB 2; Length 333;
Best Local Similarity 87.5%; Pred. No. 7.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HOYLRSPPY 8
Db 199 HSYLRSPY 206

RESULT 4
CRDL_MOUSE ID CRDL_MOUSE STANDARD; PRT; 447 AA.
AC Q920C1; Q924K0; Q9EP29;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chordin-like protein 1 precursor (Neuralin) (Ventropilin).
GN Name=Chrd11; Synonyms=Nrln1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC STRAIN=C57BL/6J;
RX MEDLINE=21334726; PubMed=11441185; DOI=10.1126/science.1058379;
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